

Docket No. CL001201DIV  
Application Serial No. TBA  
Inventors: Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEIN...

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1 GCGCCTGGGG ACCGCAGAGG TGAGAGTCGC GCCCGGGAGT CCGCCGCTG
51 CGCCAGGATG GAGTTCGTGA AATGCCCTGG CCACCCGAA GAGTCTTACA
101 ACCTGGTGCG CTTCCGGATC GGGGGCAAGC GGAAGGTGAT GCCCAAGATG
151 GACCAGGACT CGCTCAGCAG CAGCCTGAAA ACTTGCTACA AGTATCTCAA
201 TCAGACCAGT CGCAGTTTCG CAGCTGTTAT CCAGGCGCTG GATGGGGAAA
251 TGCGCAAGCG AGTGTGCATA TTTTATCTGG TTCTCCGAGC TCTGGACACA
301 CTGGAAGATG ACATGACCAT CAGTGTGGAA AAGAAGGTCC CGCTGTTACA
351 CAACTTTTAC TCTTTCTTTT ACCAACCAGA CTGGCGGTTT ATGGAGAGCA
401 AGGAGAAGGA TCGCCAGGTG CTGGAGGACT TCCCAACGTA CTGCCACTAT
451 GTTGCTGGGC TGGTCGGAAT TGGCCTTTCC CGTCTTTTCT CAGCCTCAGA
501 GTTTGAAGAC CCCTTAGTTG GTGAAGATAC AGAACGTGCC AACTCTATGG
551 GCCTGTTTCT CGAGAAAACA AACATCATCC GTGACTATCT GGAAGACCAG
601 CAAGGAAGAA GAGAGTTCTG GCCTCAAGAG GTTTGGAGCA GGTATGTTAA
651 GAAGTTAGGG GATTTTGCTA AGCCGGAGAA TATTGACTTG GCCGTGCAGT
701 GCCTGAATGA ACTTATAACC AATGCACTGC ACCACATCCC AGATGTCATC
751 ACCTACCTTT CGAGACTCAG AAACCAGAGT GTGTTTAACT TCTGTGCTAT
801 TCCACAGGTG ATGGCCATTG CCACTTTGGC TGCCTGTTAT AATAACCAGC
851 AGGTGTTCAA AGGGGCAGTG AAGATTCGGA AAGGGCAAGC AGTGACCCTC
901 ATGATGGATG CCACCAATAT GCCAGCTGTC AAAGCCATCA TATATCAGTA
951 TATGGAAGAG ATTTATCATA GAATCCCCGA CTCAGACCCA TCTTCTAGCA
1001 AAACAAGGCA GATCATCTCC ACCATCCGGA CGCAGAATCT TCCCAACTGT
1051 CAGCTGATTT CCCGAAGCCA CTACTCCCC ATCTACCTGT CGTTTGTCAT
1101 GCTTTTGGCT GCCCTGAGCT GGCAGTACCT GACCACTCTC TCCCAGGTAA
1151 CAGAAGACTA TGTTCAAGT GGAGAACACT GATCCCAAAT TTGTCCATAG
1201 CTGAAGTCCA CCATAAAGTG GATTTACTTT TTTTCTTTAA GGATGGATGT
1251 TGTGTTCTCT TTATTTTCTT CCTACTACTT TAATCCCTAA AAGAACGCTG
1301 TGTGGCTGGG ACCTTTAGGA AAGTGAAATG CAGGTGAGAA GAACCTAAAC
1351 ATGAAAGGAA AGGGTGCCCT ATCCCAGCAA CCTGTCCTTG TGGGTGATGA
1401 TCACTGTGCT GCTTGCGGCT CATGGCAGAG CATTCACTGC CACGGTTTAG
1451 GTGAAGTCGC TGCATATGTG ACTGTCATGA GATCCTACTT AGTATGATCC
1501 TGGCTAGAAT GATAATTAAA AGTATTTAAT TTGAAAAAAA AAAAAAAAAA
1551 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
1601 AAAAAA (SEQ ID NO:1)

```

**FEATURES:**

5'UTR: 1-57  
Start Codon: 58  
Stop Codon: 1180  
3'UTR: 1183

**Homologous proteins:**

Top 10 BLAST Hits

	Score	E
CRA 108000024649260 /altid=gi 12734163 /def=ref XP_005134.2  fa...	770	0.0
CRA 18000004925908 /altid=gi 4758350 /def=ref NP_004453.1  farn...	743	0.0
CRA 18000004929946 /altid=gi 2135096 /def=pir  I38245 farnesyl-...	741	0.0
CRA 18000004993865 /altid=gi 2136196 /def=pir  I52090 squalene ...	740	0.0
CRA 18000004932414 /altid=gi 6753838 /def=ref NP_034321.1  farn...	671	0.0
CRA 18000004937535 /altid=gi 9506591 /def=ref NP_062111.1  farn...	654	0.0
CRA 1000682330885 /altid=gi 6002565 /def=gb AAF00038.1  (AF0903...	582	e-165
CRA 335001098694081 /altid=gi 11514495 /def=pdb 1EZFA Chain A,...	579	e-164
CRA 18000005103884 /altid=gi 2463565 /def=dbj BAA22557.1  (AB00...	282	1e-74
CRA 18000005103885 /altid=gi 7434086 /def=pir  T00489 farnesyl-...	280	4e-74

FIGURE 1A

BLAST dbEST hits:

	Score	E
gi 12926380 /dataset=dbest /taxon=960...	1441	0.0
gi 12945082 /dataset=dbest /taxon=960...	1370	0.0
gi 12921315 /dataset=dbest /taxon=960...	1346	0.0
gi 11642571 /dataset=dbest /taxon=96...	1330	0.0
gi 9141948 /dataset=dbest /taxon=9606...	1281	0.0
gi 13040072 /dataset=dbest /taxon=960...	1233	0.0
gi 12944143 /dataset=dbest /taxon=960...	1055	0.0

**EXPRESSION INFORMATION FOR MODULATORY USE:**

library source:

From BLAST dbEST hits:

gi|12926380 placenta  
gi|12945082 T cells from T cell leukemia  
gi|12921315 Fetal brain  
gi|11642571pancreas  
gi|9141948 Burkitt lymphoma  
gi|13040072 bladder

From tissue screening panels:

Whole liver

FIGURE 1B

1 MEFVKCLGHP EEFYNLVRFR IGGKRKVMKP MDQDSLSSSL KTCYKYLNQ  
51 SRSFAAVIQA LDGEMRNAVC IFYLVLRALD TLEDDMTISV EKKVPLLHNF  
101 HSFLYQPDWR FMESKEKDRQ VLEDFPTYCH YVAGLVGIGL SRLFSASEFE  
151 DPLVGEDTER ANSMGLFLQK TNIIIRDYLED QQGGREFWPQ EVWSRYVKKL  
201 GDFAKPENID LAVQCLNELI TNALHHIPDV ITYLSRLRNQ SVFNFCAIPQ  
251 VMAIATLAAC YNNQOVFKGA VKIRKGQAVT LMMDATNMPA VKAIYQYME  
301 EIYHRIPDS PSSSKTRQII STIRTQNLPN CQLISRSHYS PIYLSFVMLL  
351 AALSWQYLTT LSQVTEDYVQ TGEH (SEQ ID NO:2)

**FEATURES:**

**Functional domains and key regions:**

[1] PDOC00001 PS00001 ASN\_GLYCOSYLATION  
N-glycosylation site

Number of matches: 2

1 48-51 NQTS  
2 239-242 NQSV

[2] PDOC00005 PS00005 PKC\_PHOSPHO\_SITE  
Protein kinase C phosphorylation site

Number of matches: 5

1 39-41 SLK  
2 50-52 TSR  
3 158-160 TER  
4 313-315 SSK  
5 322-324 TIR

[3] PDOC00006 PS00006 CK2\_PHOSPHO\_SITE  
Casein kinase II phosphorylation site

Number of matches: 3

1 81-84 TLED  
2 145-148 SASE  
3 147-150 SEFE

[4] PDOC00008 PS00008 MYRISTYL  
N-myristoylation site

Number of matches: 2

1 137-142 GIGLSR  
2 276-281 GQAVTL

[5] PDOC00009 PS00009 AMIDATION  
Amidation site

22-25 GGKR

[6] PDOC00802 PS01044 SQUALEN\_PHYTOEN\_SYN\_1  
Squalene and phytoene synthases signature 1

128-143 YCHYVAGLVGIGLSRL

[7] PDOC00802 PS01045 SQUALEN\_PHYTOEN\_SYN\_2  
Squalene and phytoene synthases signature 2

164-189 MGLFLQKTNIIRDYLEDQQGGREFWP

FIGURE 2A

**Membrane spanning structure and domains:**

Helix	Begin	End	Score	Certainty
1	125	145	0.834	Putative
2	241	261	1.467	Certain
3	339	359	1.716	Certain

FIGURE 2B

**BLAST Alignment to Top Hit:**

```
>CRA|18000004925908 /altid=gi|4758350 /def=ref|NP_004453.1|
    farnesyl-diphosphate farnesyltransferase 1;
    Farnesyl-diphosphate farnesyltransferase 1 (squalene
    synthase); Squalene synthase [Homo sapiens] /org=Homo
    sapiens /taxon=9606 /dataset=nraa /length=417
    Length = 417

Score = 743 bits (1898), Expect = 0.0
Identities = 374/417 (89%), Positives = 374/417 (89%), Gaps = 43/417 (10%)

Query: 1   MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYLNQTSSRFAAVIQA 60
          MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYLNQTSSRFAAVIQA
Sbjct: 1   MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYLNQTSSRFAAVIQA 60

Query: 61   LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120
          LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ
Sbjct: 61   LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120

Query: 121  VLEDFPT-----YCHYVAGLVG 137
          VLEDFPT                      YCHYVAGLVG
Sbjct: 121  VLEDFPTISLEFRNLAEKYQTVIADICRRMGIGMAEFLDKHVTSEQEWDKYCHYVAGLVG 180

Query: 138   IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV 197
          IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV
Sbjct: 181   IGLSRLFSASEFEDPLVGEDTERANS MGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV 240

Query: 198   KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCaipQVMAIATL 257
          KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCaipQVMAIATL
Sbjct: 241   KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCaipQVMAIATL 300

Query: 258   AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEIYHRIPSDPSSSKTR 317
          AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEIYHRIPSDPSSSKTR
Sbjct: 301   AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEIYHRIPSDPSSSKTR 360

Query: 318   QIIISTIRTQNLNPNCLISRSHYSPIYLSFVMLLAALSWQYLTTLTSLQVTEDYVQTGEH 374
          QIIISTIRTQNLNPNCLISRSHYSPIYLSFVMLLAALSWQYLTTLTSLQVTEDYVQTGEH
Sbjct: 361   QIIISTIRTQNLNPNCLISRSHYSPIYLSFVMLLAALSWQYLTTLTSLQVTEDYVQTGEH 417 (SEQ
ID NO:4)

>CRA|108000024649260 /altid=gi|12734163 /def=ref|XP_005134.2|
    farnesyl-diphosphate farnesyltransferase 1 [Homo
    sapiens] /org=Homo sapiens /taxon=9606 /dataset=nraa
    /length=431
    Length = 431

Score = 743 bits (1898), Expect = 0.0
Identities = 374/417 (89%), Positives = 374/417 (89%), Gaps = 43/417 (10%)

Query: 1   MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYLNQTSSRFAAVIQA 60
          MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYLNQTSSRFAAVIQA
Sbjct: 15   MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYLNQTSSRFAAVIQA 74

Query: 61   LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120
          LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ
Sbjct: 75   LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 134

Query: 121  VLEDFPT-----YCHYVAGLVG 137
          VLEDFPT                      YCHYVAGLVG
Sbjct: 135  VLEDFPTISLEFRNLAEKYQTVIADICRRMGIGMAEFLDKHVTSEQEWDKYCHYVAGLVG 194
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**FIGURE 2C**

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Title: ISOLATED HUMAN ENZYME PROTEIN...

Query: 138 IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV 197  
IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV  
Sbjct: 195 IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV 254

Query: 198 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAPQVMAIATL 257  
KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAPQVMAIATL  
Sbjct: 255 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAPQVMAIATL 314

Query: 258 AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR 317  
AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR  
Sbjct: 315 AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR 374

Query: 318 QIISTIRTQNLPCQLISRSHYSPIYLSFVMLLAALSWQYLTLSQVTEYVQTGEH 374  
QIISTIRTQNLPCQLISRSHYSPIYLSFVMLLAALSWQYLTLSQVTEYVQTGEH  
Sbjct: 375 QIISTIRTQNLPCQLISRSHYSPIYLSFVMLLAALSWQYLTLSQVTEYVQTGEH 431 (SEQ  
ID NO:5)

>CRA|18000004929946 /altid=gi|2135096 /def=pir||I38245  
farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21),  
hepatic - human /org=human /taxon=9606 /dataset=nraa  
/length=417  
Length = 417

Score = 741 bits (1893), Expect = 0.0  
Identities = 373/417 (89%), Positives = 373/417 (89%), Gaps = 43/417 (10%)

Query: 1 MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYNQTSRSFAAVIQA 60  
MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYNQTSRSFAAVIQA  
Sbjct: 1 MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYNQTSRSFAAVIQA 60

Query: 61 LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120  
LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ  
Sbjct: 61 LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQ 120

Query: 121 VLEDFPT-----YCHYVAGLVG 137  
VLEDFPT YCHYVAGLVG  
Sbjct: 121 VLEDFPTISLEFRNLAEKYQTVIADICRRMGIGMAEFLDKHVTSEQEWDKYCHYVAGLVG 180

Query: 138 IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV 197  
IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV  
Sbjct: 181 IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDDQGGREFWPQEVWSRYV 240

Query: 198 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAPQVMAIATL 257  
KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAPQVMAIATL  
Sbjct: 241 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAPQVMAIATL 300

Query: 258 AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR 317  
AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR  
Sbjct: 301 AACYNQVFKGAVKIRKGQAVTLMMDATNMPAVKAIYQYMEEIYHRIPSDPSSSKTR 360

Query: 318 QIISTIRTQNLPCQLISRSHYSPIYLSFVMLLAALSWQYLTLSQVTEYVQTGEH 374  
QIISTIRTQNLPCQLISRSHYSPIYLSFVMLLAALSWQYLTLSQVTEYVQTGEH  
Sbjct: 361 QIISTIRTQNLPCQLISRSHYSPIYLSFVMLLAALSWQYLTLSQVTEYVQTGEH 417 (SEQ  
ID NO:6)

FIGURE 2D

Hammer search results (Pfam):

Model	Description	Score	E-value	N
PF00494	Squalene and phytoene synthases	425.8	4e-124	2

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00494	1/2	47	126 ..	1	88 [.	124.6	1.1e-33
PF00494	2/2	127	291 ..	146	317 .]	301.1	1.3e-86

FIGURE 2E

```
1  TATTTATTCC TAATTAAATG GGGAGGAAAG TCTTTGAAGA GGAACCTCTA
51  CTTTACTTTT TATACCGTCA TGGCTGGAAA CTAAGTTTTT AAGATTTTTT
101 TGGGGTCCCG TTGGCCGAGG TGGGGAGTGG GAGGGCTGTC CAGTGGTAGG
151 GACTTAGGAT TTTTAGTTTA CAGTAGTAGG GGAAACACTC TGTAATCTAA
201 TACATAAGTA AATGATGTAT TAGAATATGG TAAATATAGG CAAGTAGACC
251 CCCACTGGGA TTAGCAGTGG TGGAAATGTG AGAGAGGGCA AACAGGTGGG
301 TCTAGATGAG GTGTGAGCAG ACTCGAGGGG CACAGGAGTT AGTCAAGCCA
351 GTATCTGGGG GATAGTGACG GAATAGTGAA CAGCTAGACA AAAAGTCCTA
401 GGGCCAGAGA AAGCAAAAGC ATAAGAGATG GAGGCCAGAG AGGTAATCTG
451 GGTGGAAGGC TGCAGCCTCT CAGGATCCCT ATAGGTGCTT TGGCTTTTGT
501 TGGAGAGACA CTGAACAGCT TTGGGCAGTG AACGTACCTG ACAGGTTTCC
551 TGTTTGTTTT TGAGATGAAG TCTCGCTCTT GTCCCCCAGG CTGGAGTGCA
601 ATAGCGCGAT CTCAGCTCAC TGCAACCTCT GCCTCCTGTG TTCAAGCGAT
651 TCTCCTGCCT CAGCCTCCCA GGTAGCTGGG ATTATAGGCG CCTGCCACCA
701 TGCCTGGCTA ATTTTTGTAT TTTTAGTAGA GACGCAGTTT CAGCATGTTG
751 GCCAGGCTGG TCTTGAACCT CAGACCTCAG GTGATCCGCC CGCCTTGGCC
801 TCCCAAAGTG CTGGGATTAC AGGCGTGAGC CACCGCGCTC GGCTAGACCT
851 GACAGGTTTT AAAAGGATTA CTGGTTGCTG TGTTAAACA GACTGCAGGA
901 TGGCTTAGGT AGCCAGTAGG TTTTTTTTTT TTTTGGAGAC GTAGTCTTGC
951 TCTGTTGGCC TGGCTGGAGT GCAGCGGTGT CATCTTGGCT CACTGCAAAC
1001 TCCGCTTCCC GGGTTCAAGT GATTCTCCTG CCTCAGCCTC CGGAGTAGTT
1051 GGGACTACAG GCGCCACCA CCACACTCGG CTTTTTTGTA TTTTATAGTAG
1101 AGACGGGTTT CACCATGTTG GCCAGGATGG TCTCGATCTC TTGACCTCGT
1151 GATCCACCCG CCTTGGCCTC CCAAAGTGTT GCGATTACAG GCGTGAGCCA
1201 CCACGCCTGG ACGGGTAGCC AGTAGTTTCT AGGGCTGGAG AGATCTAGGA
1251 TGAGAGAAAT TCCACATTC CTGTTACAGG CTCTCTAAGG CTTCAGCTCC
1301 TTTTCTAGG ACTAAGCTGG ATCTCAAGTA AACACTAGAG AGGGGCGAGC
1351 TGAAGCTCCA GGAGTGTGTG GGGCTCCCTG GGGCTGGATG GCGGTGGCGG
1401 GCAGGCGAGC TGGGCTGTGC TCGGGTGTGT TACAGTAAAG ACGCCCAGCT
1451 TGGCGCTGGC CCGGCCTTTT CACGGTTTTA GGCTCTACAG AGAGCGGCTG
1501 CAGAGCTCAC CCGGCTGGCA GGAGCCACCG AGGCCGAGCA CGTGGGCGAC
1551 TTATTGACCA AGTGGGGAGG AAGCAGCCCC GCACTGCTCT CCCGACTGCG
1601 GACCACCGTT GGGCTCATGC GCATCATAAG CCCCACCGCC TCACCTCCAG
1651 TCCCCACAGC GTTCGCGCTC CCAGCCGGGG TAAGCGGAAG AAAACAAAGG
1701 CCCGGCTCCA TCAGGGCACC AATCCCGCTC GTCGGCCTCT TTCTCGGCCT
1751 CCAATGAGCT TCTAGGGTGT TATCACGCCA GTCTCCTTCC GCGACTGATT
1801 GGCCGGGGTC TTCTAGTGTG GAGCGGCCCT GGCCAATCAG GCGCCCGTCA
1851 GCCCACCCCA CGAGGCCGCA GCTAGCCCCG CTGGCGGCCG AGGCCGGTTG
1901 AAGTGGGCGG AGCGGCGGGC GGGGCGTCGC CGTACTAGG C TGCCCCCTG
1951 TCCGCGCAGC CCTCGAAGC ACCTACTCCA CAGGTCCAGC CGGCCGGTGA
2001 GCGCCTGGGG ACCGCAGAGG TGAGAGTCGC GCCCAGGAGT CCGCCGCTG
2051 CGCCAGGATG GAGTTCGTGA AATGCCTTGG CCACCCCGAA GAGTTCTACA
2101 ACCTGGTGCG CTTCCGGATC GGGGGCAAGC GGAAGGTGAT GCCCAAGATG
2151 GACCAGGTGG GCCGAGCCTC CCTGCTTGCC CGGGGCGGGG AAGGAGCTCG
2201 CTGGGCCGGC CTCAGGGCCT GAGCGGCCCG GCCCGATCT GGGGCAAGGG
2251 GCGCGCGAG CAGGGCCGAC GCCTGGGTGT TCCCGTCCCC CTTTCTCGA
2301 GCCTTCCCC TGTAGGGCCC GGGTGGACGC GGCCGTCTG GCTGACCTGT
2351 CCCTGCCCC GCAAGCCGCC CTGGGCATGA GCGACTTTTG CGTGGTTCCC
2401 GGTGGTTGCG CTCCCCGTTT CGTCCCCTCC GTGAGCATCG GCGCTTACCG
2451 GTATTTTAAC CCGAGGGTTA CACATCTGAG GCAATGTGGG TGGGTTACGC
2501 GGGAGAGGAC GAGTGAGTTT TTTGGTAAGC GGAATGAACT ATGCAGATAA
2551 CATCATGA AGGCCGTTT TGAATGAAG TCTGACTCCT CCAGTTTAC
2601 CACCTCTTCC GGAGCTCTCC CCGCCTTGCT GCCTTCCATC GCTTCATCCT
2651 CGGTGCTTCC TGAGTTTTAA AATCGCCTAT CTACGCTTCC AAGTTCCAAT
2701 GAGTTATCTA ACGTCTATGG ATTAGCTAGG TGGTTGGTGG AAGGTCAGAA
2751 CTTGGTTTTA CTTAGATTTT TATCTGCCTC ATGCCTGTAC TATTGTTTA
2801 ATGAATGCAT AGGAGGTGTT TTTATTCCAA CAAGAAATT ATTCTGACGC
2851 GATTATTGAA TGAATAGACA AATTGAGCCA AGTTCTTCTG GTCTGGACCA
2901 GCCTGGCTGA TTTCTGTAAC TTTTGGGC CAACAGGACA GTAGCAAATG
2951 TGACTCAGGC CGAGGCTTGA TAGGTGCCTG AACATCGAG TCTTCTTTC
3001 AGTGTCCATG TGCTTCAGTA AACACACTAG AAAATAAATT TCTGGTTTTT
3051 GTCCCCAGTA GACTACACCC TCATTTGGTG TTATTTTCA CGTGCTATCT
```

FIGURE 2A



```

3101 TTAATACAGG TACATCCTTC AGTCTATTTC TAGAACATTC AGTTTCTCTC
3151 ATCTTTTCTT TGCCGGTGCT ACATTATTTC AATTATTTTC CTACAGAATA
3201 ACTTCTATTA TTTGATATGG CAGATGTCAC TTTTATATAT TAGATATAGC
3251 ATTCATTTAT TTAACAAATA TTTGACGACC AGTTGTATAT CAGATAGTGT
3301 TCTAGGTGCT GGAGGTACAA CAGTGAACAA GCTAGGTGAA GACCTTGATT
3351 TTATAAAACT TACTTTTTAG TGGAAGAGAG ACAATTTAAA AAAGCGAATG
3401 TACAGTTTTT CACGTGGAGA AAAGCACTGC AGAGGAAGAT ACTAGCAGGG
3451 CAAGGGATCT GAGTGCAGTC AGACCTCATT TGGGTCCAGA CTTCAATCCT
3501 CTATGTCTCT TTCCTTTCTA CAGAAAGACT GTTAGAGAAA ATGGTAGCAT
3551 TGGTTTCCTG TTGGGAGGGA AAGTGGGTGG TCATGGTAAG TGGGTAGAGA
3601 AAGACTTCAC AGTATACTGT TTTTGTACAT TTTGAGTTTT TTTAAAAGCG
3651 AGACTTGAGC TATTCTAGCT CTGATAATAT GGTGCAGTAT TTGTTATGTT
3701 AGTTGTAGTC TTTCTGGGCA GTTTTTACAT CCCCATGAGC CGTTAAAAAA
3751 ATACCTGAAC CTTTAAATAG GGGAAATAAA TTGGAAAAAT ACATTCCCTT
3801 TCACTTAACA TTATCTTAGT TTCTCTTTTT TTTTTTTTTT TTTTTTGAGA
3851 TGGAGTCTTG CTCTGTTACC CAGGCTGGAG TGCAGTGGTG GCGGGACCTC
3901 AGCTAGATGC AGCCTCCGCC TCCTGGGTTC AAGCAATTCT CCTGCCTCAG
3951 CCTGCTGAGT AGCTGGGATT ACAGGCACCT GCCACTACGC CCGGCTGATT
4001 TTTTGGTATT TTTAGTAGAG ACGGGGTTTC ACCATGTTGG CGAGGCTGGT
4051 TTTGAACTCT TGACTCAAG TGATCTGCTC GCCTTGGTCT CCCAAAGTGC
4101 TAGGATTACA GGCGTGAGCC ACTGCACCCG GCCTTTTTTT TTTTTTTTTT
4151 GAGGGGGGGG TCTCACTCCA TCGTCCAGGC TAGAATGCTG TGGCCTGAAC
4201 ATGACTCACT CCAGTTTTGA CTTCTTGGC TGAAGCCATC CTCCCACCTC
4251 GGCTTCCTGA TCCCGAGTAG CTGGGACTCC AGGCACGTGT CACCAATGCA
4301 TGGCTAATTT TTAAATTTTT TTGTAGACAC AATGTCTCGC TGCATTGCCC
4351 AGGCTGGTCT TGAACCTCTG AGCTCAAGCG ATTTTCCCAC CTCAGCCTTC
4401 AAAGTGCTGG GATTACAGGT GTGAGCCACT GCACCAACC AGTTTCTCTC
4451 TGCAAACCTAG GGAAAAAATT TACGCTTAGC AGATATTGAG GGCTGATTAT
4501 TTCTATCACA GAAGCATTTG GCTATAGAAT TTCAGGGTTT AGTAAACTTG
4551 ATTTACACTG AATTTTTAGG TGCATATCAG TAAATCTACG GGCATATGCC
4601 GCCTGCAAGT TGTGTGGCAT CACCCAAAAG CCGAGAGTAA TGGAAAGAGC
4651 AGGCTGTTAG TAATCAGGCA GATCTGGCTC CTGTCCAATC TAAATCCTGT
4701 TATTTAGACT AATATCTTAA GTCTGTTATT AAGTCCGATT TCTGACGCTA
4751 TTAAGTTAGG TGAACACCTT TGGTAACTTA ACCTCTGAAC CACAGTTACT
4801 TCATCTGTAA AATAGGGATG TATGTATGGT AACGATTTTT TAACCACAAC
4851 TTCCCAACTC TAAGATGGTC TGAAAAGAAT TTTTGTAGTG TTTGGCTCAG
4901 AATCACTTGG CAGCAAAACC TGACTTGAAG TTGAGGCTTC ATTCAATCCA
4951 CTTAGTATAT TCAAATGTTT TGCTAAAGAA ATAATTATGA GGTGCTACTT
5001 CACACTGACT AGGGTTGTAT ATGCATTTTA TTGCCTATTT TCTAAAACAC
5051 TAAAAATGCT AAATTTCTGCC CCAGGTCTTG CCACAGATGT TTCAGTGGAC
5101 TATGGGCCCTG TGAGACCTTA AAGGGTTGAT TGAGTAAGGA TCACAGGTGA
5151 TGTCCGCATT GTGCTTGGCA TGGAGTTAAG TGCTTGATAA ATGGTGGTTA
5201 TCAATCTGAT TATGTAAATT TATGTAAATT CAGTTCTCAA GTTTGTGGTT
5251 TTTTCCCTCT CCTGGAGAAA TCTATTCTAT TTTAAAGTGA GGAAGGCTCC
5301 GTGGAGGGCT GGTAGCTGGT AGCTGTTTAC TTGTGGAACT TTCAGCCTGA
5351 GGCTGGAGCC CCTTCTGGG AGTCTGGTCT TGTCGTCTTC CTGACCACCC
5401 CCACACCCTT CCTTAAATT CCCTCCATCC CTGTTTTTCT CCCGCTTGCG
5451 AGCTTTTGGG AGTGTGCTGA ATCTCAGACT GCAATAGATA AACCCAAGAG
5501 GGACAGGCAC CAGTAGCCTG AGCTTGCTTT CTCCCCTGGC TCATGGGAAT
5551 CAAGCAGTAG AAATTTTTAG TGAGTGTGTG TTTCCATAGT ATGCTTACTA
5601 GTTGTGTCTT CTGTTTTGTG TCTTGGTGAT TTGAAGAAAC CTGTTTACAA
5651 GGTAAGGGAC TGAAACAAAT AGGTGACAGG AAAAAGAGCA GCAGGGGTAC
5701 GAGCTGGAGG AGTAAGTGGC TTGGCTTGCT CTCTTTCAGA ATGGAGGGCT
5751 GTATGGAAAG GAGGGTAGT GTTCTTGAAG AGTGTGGGG TTTAAATCTA
5801 GGGGGACCGT GTCTTGGCAT TGATTGAAAC TCCTGGCTTA ACATCACCCC
5851 GAACTGTGA GTTGGACTGA ACATGACATT TGGCAGTGCA GTTAAAAACA
5901 CTTCTGTCTG TAGCCTGGTA ATGGTCAGGC TATGTGAAGA GCTGCTCTGG
5951 AGCTCAGTCC AGAGCGGTA TTCTGTTTCT TTCACTCTGA AATCCTGCCT
6001 CTCGATATTT TGAGAAGGAA GGAGTTGGTG AATTGTTTTA AAATCCTCGA
6051 TGAATGTCTT CATTTATTC TACACCACT TCTGAATATA TTTATGTGCC
6101 AGACGCTGAA GTTTACTAAT ATTATGGTGC CCAGTAAATA CTTGTTTTTA
6151 CTAATATTTT TTATGGCAAT AAAATGACTT TTTCAGGATT ATGTGATTTA

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FIGURE 2B

Docket No. CL001201DIV  
Application Serial No. TBA  
Inventors: Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEIN...

6201 AAAGATTGAC CCTTTTGGCA AAATACGTAT TCATGATAGG AAATATATAC  
6251 AACATAGTTC ACTTAAACCT CCCACCAGAG CCCAGGGTTC ACTGTTACCA  
6301 TTCTGAAGTG ACTGGAATTT CCTAGAAGTG GATATGCCAT ATTTTTTTAA  
6351 CCACTCCTAT TGGATATTTG TTTTTTATTT TTTTGAGATG GGGTCCCACT  
6401 CTGCAGTGTA CAATATCATA GTTCACTGTA ACGTGTATCT CTTGGGCTCA  
6451 AGCGATCCTC CCCACCTCAG CCTCCCTGAG TAGCTAGTCT TCAGTAGCTA  
6501 GACTATAGGT GGGCGCCACC ACAGCTGGCT TTTTAAAAAA TTTTTTATGA  
6551 ACACGAGGTC TCACTATGTT GCCCAGGCTG CCCTCAAACCT CCTGGGCTCA  
6601 AGTGATTCTC CCACCTTGCG CTTCCGAAGT GCAGGGATTA TAGGCGTGCG  
6651 CCACTGCACC CGGCCCTGTT GGATAAATGA TTCCAGTCTC TCCCAAAAAG  
6701 AACTGTTGTA AGACTGTGGG GTGAGGGGAG GGAAGGGACA AATAGGAACC  
6751 CGCCGTATTT TCCACTCCCT GTGGGCCTAA AACTGCTCTA AAAAATAGTC  
6801 CATGAAAAAA TACATAGTAC AAACAGCAAC TCTTTCTGAT ATGCTTGCA  
6851 TTAAAAACAG GCTTTTTCTC CCTTTTGGAA AAACACAGTC CTTGTTTGCT  
6901 TTAGGGAAGA GTAAAGGTCA GTGCGCTGCA TTGCATTAAT TTCGAAGGGA  
6951 AAGATGAGAA GACATCTTGA AAGGAATGGC TGGCTTTCTA GAGAATAGTA  
7001 GAGGCTTAAT AGGTGTCATA GAAAAACCAG GGTTGGACAG TGGTAGTAAA  
7051 ACGGCAAAAC AGATTTTATT CAGAAAAACT ACTGCAGTAA GAGGAGAGAG  
7101 ACCTCGGTAC AGAAGTGCCT CACTGCGAAT ACAAAGAAAA GTAGGAATTG  
7151 ATGGCGGGGG AGCCGGATGT CAGTGGATGG AAAATTATTA CGAGGAAACA  
7201 CAGGGGTGTG CATTCTTGCT GAAGGCAGGC CAGAGTTATC AGACATCACC  
7251 TGAGGGATGG AGGGGGATGT GGAACCTAAT CGGCTGTCTA GGGTGATCAG  
7301 ATACTGAAGT TGGGGGATTC TGGTCAAATC AATTTAGCAG GATTCTTGGT  
7351 AAAACTGGGC GATGCAAAGA CAGATGCGTT GAGTACAAAG TCCAGGCTTT  
7401 ATTGGGAAGA GGATTTACAG GGAGCCCGAG TAGAGTTTGG TCTAGGGAGA  
7451 CTCTGTCACT GGGAGGACGA GCGAGCCGCT CGGAAGTGCG CTGGGTCTC  
7501 TTAGCGGCCA GTGGGTCTG GTGAGAAGGG CAACAGCGGG AGGAGGCGCC  
7551 GGTGCGGAGC GGGAGGCCGG GGGCGGGGCT GCGGGGCTGC GGGGCGGGCC  
7601 CGTTGTGGGT CGGCCAGCG CGTATTCGAG TAGAGGGCGA GCCCGTCCCG  
7651 CCTCTCGTCG GCGCTTCCC AGATCTGCTT GAGTCTATGG AGGAAAAACT  
7701 CCGCGGGGTC CGCGATTCCC ATGGCCGCG CCGCTGCGG CACCAAGGCC  
7751 ATGGCCCTCT TCAAGCGCAC CTTGGTGTG AGTCCCGCG CGGCGCCAG  
7801 GGGCCCGGGC CAGGCACCG CCCC CGGGG CTGCTGCTTG CCTCTGCCC  
7851 CCTGGCCCTG CAAGGACTGG CCTCGGGAG AGGGCGGCAG GCTGTGGAGC  
7901 CGCCTGCCCC AGTCCAGTC CCACTCCAC TCCACTCCC ACTCCCACTC  
7951 CTGCTCCTCG ACGTCTCCCA CCGCCGTGTG TGTGTCTGC CCGCAGGACT  
8001 CGCTCAGCAG CAGCCTGAAA ACTTGCTACA AGTATCTCAA TCAGACCAGT  
8051 CGCAGTTTCG CAGCTGTTAT CCAGGCGCTG GATGGGAAA TGCGGTGAGT  
8101 GATGGAGGCA GCGCCTCTGG CTTGGAGGAA AGCTTGTCGG GGAATTTTGA  
8151 GTGTGTTGGA AGCTACCTTT TGATATAGCG CTCAGCGTTG CAGCCTCGTT  
8201 GCTGTGGCTT ATCCAGAACA TAGCCCGGCC CTACGTGTTT ACTTTAGAAA  
8251 GCCCTTCCAG GCTCTTTGCC ATCTAGTAGA GTCCCTGCGG GCCCAGCCTT  
8301 TCAGAGAAGG GGGGGGAGGG GGTGATGTTT ATTAACTTT TTTAGTCTTG  
8351 GCAGCTGAAC CTGCTGTGA GCAGGTCGTG TATTTCTCGG CTTCCCTTAT  
8401 CCAACTTTGC ATTTCTATTT CTAGCATATT GGGTTGATTC TTTTGAAGCT  
8451 GCCTCTGTGC ACATTACACC CATGAACCTA GACCAGTTGC CTTTATGTAT  
8501 GATCGTATTT ATACTGAGAA GTTACTGTGT TTTTGTACTT TCTTTTCTAT  
8551 TTGCTACATA TTAGTTCGGT CTAAACGTTT GGTCTTCTGG TCTCCATAGT  
8601 TCTACATTGG TTAAATGCAA CTCACCTCTG GGAGTAGTGG TGACATTCAA  
8651 CTAGTAGGCT TTTTAATAAA CTACAGAAGT TCATTACTCT CATGTAAGGA  
8701 AGGAAAACTA ATGTAACCTT CGTTAAGTAT GAAAAGCGTT GGATATCCTT  
8751 ATAGTTCTTT AGAGTTAAGG GTGAGATGGG TTTAGAAAGT GGCCAGGCAC  
8801 AAGTTATTTT AAAATAAAAA ATCTTTGGCT GTTTGTTCCA ATATATTAAT  
8851 AGTTTTCCCT TTTTACAGC AACGCAGTGT GCATATTTTA TCTGGTTCTC  
8901 CGAGCTCTGG ACACACTGGA AGATGACATG ACCATCAGTG TGGAAAAGAA  
8951 GGTCCCGCTG TTACACAAC TTTACTCTTT CCTTTACCAA CCAGACTGGC  
9001 GGTTCATGGA GAGCAAGGAG AAGGATCGCC AGGTGCTGGA GGACTTCCCA  
9051 ACGGTGAGTG GGGTTACGCA TCTTGTCTAC GGACTGTTGT GTTCATAATT  
9101 GCTAACGTGG TTGTCCGTA GCCTCCATAC ATGTGGAGAA AGGTTAAATA  
9151 AGCATTCTGA GGCAGCATA ATGTGAGGAT TAAAAACTCC GGTAGCCAAG  
9201 ACTCTGAAGC CAGGCTGCCT GGGTTGGAAT CTCAAATCTC CCACTTACTA  
9251 AACTGTTGGT TACTTACAAA GACTCTCTGT GCCTCAGTTT CTTTCATCTGT

FIGURE 2C

9301 AAAATAGGGG TAATAATAAC ACCTACCTCA TGGTATTCTG AGGATTCAAA  
9351 GAATTAACGT AGGTAATGCT CTTAGAATGT TAGCTACTGC TGTATTATATC  
9401 AGTATTGGAA GTCCAGTGTT TCTTCCTGTG GGAAGACGCA GTCAAATTTT  
9451 AGTGTGTGTA AAGATTCTCA GGCTAGCTCA CAAAAGCCTG CCGACTGTAT  
9501 GATGCAGCCT ACCTGTAACA CTGCTGGCCT CTTGACTACC CGGAGCCTGG  
9551 TAGCATGGGA CTGCTGCTCA CGATGGGCAG CAGCCTGGCA TGGGGGCGGT  
9601 GTCTGTTGGC AGCTAGGGCG AGCCTCTGCC ACTTCACCTG TGATCCTGGG  
9651 CAAGTTCCTT ATCTGCTTTG TGTCTCCGTC TCCTCGTTTG TAAAGTTAGA  
9701 GCTGAGAGGA TTAATTTTCG ACATATAAAG TACTTAGTGC CTGGTACAGG  
9751 GTAAGTATTC TGTAAGTATT AGCTATTTGG TCTATTTTGT TGGAGTAAAG  
9801 TGGGTTATAG TTAATAATCCT AAGATTTTAA AAGTCCCTCA AGTTCACGTG  
9851 GACATCTGCC TAGGTCCTAC TATCCTAGAA TTCGCATGTC TTATCACACA  
9901 AATAATGAT TCTTCCATAT CTTATAAATA AAGGTTTGAT TTAGCAAAGT  
9951 CACATGTTGT GTAATAGCTC GAAGAAGCCC TTTTGTGTTT CAGTTGCCAG  
10001 AGCTTTTGGG GAACAGTCCT TATGTTATTG AAACAAACCT AATCTGTAGC  
10051 TGAGTTGGGA GGGAGCTAAG TGGACAGAGA GTCCTCCACC CAAACAAAAG  
10101 AATCTTTGAT TCTTGGGCAT AATGGGAGCA ATATTTAAAA AAAAAAAAAA  
10151 AAAAAAAAAA GGAATGTTTG GGGAAGACTC TTGCGGTGCA AAGGCTGTTT  
10201 CAGATTGCTG AGATCAGACC TTAAGTACCA AAGCCCAAAT ATAGTACAAC  
10251 ATAATACAAA TGAGAAGAAA ATAGCTGAAG AATAAATCGA GTTTATACAG  
10301 TACAATTCAA GAGAAGAAAG AAAATTTATG ACGACTAGCT GGGTGAGAAT  
10351 TAGAACTGTA ACCCTGGGAA GGTCTTGGTG ATTTGACTCT CACAGGACAC  
10401 CTGATGACCA GAGGATGGGT TTCCTTTGAT GGGAAATCTG TGGCGATTCA  
10451 TTGATGGGCC TCTGAATTCT GCTGAAGCAG AGGAAGTAGT AATACCCCAT  
10501 TTATAATGGA AGTGCATTCT CACTTAAAAA CAACTAATAT TATTCTAGCT  
10551 GGACCTAGCC TCTAGAAACA GCCAAATTAC ATTTGACTTG AGTGGATTCA  
10601 TAATAATTAA AAAATTTCTG GGGCATGGGA TAAATGTGTT AGGTATTGCT  
10651 AAGTCAAGGC AGCCCTATCC CCTCAGCAGA AGTGAGGGAA TATGAAAGTG  
10701 TGTGAATGCT AACATAATTT TGGGGAATAT CGCCGTCAGA TTTCCAGATG  
10751 ATATTCCAAC ATGTTTGTGA AACTTCAGTG TCTTCCTGTG TTCATACAGT  
10801 GTTCCAGTGG AAAAATAATG CTTAGTTCTG GAAGGTTTCA GATGTGAACA  
10851 CTGAACCTCAT CGTTTTCTTT TTTGGGTAGT AGAGTTAGAG ATTCCATCCT  
10901 CTTGAAAGCA CAGTTGCCCC GGGAAGAGTA AAAGGGAGCA GAAGGCGTAA  
10951 GCCAGGCACG GCTGTTTTCA CTGTTGTTCA CCTTTTGTAT CCTTACGAAT  
11001 ATGAAGATGT ACTAAGTTGT GTGTTTTGCG TGCATATATA ATTTTAAGCT  
11051 ACTTGAGTTG TAGGTCCCTC CAGTCTGTGA TTCAGTTTGA GATGGGACTG  
11101 TATGGGAATT AACAGTGCCT TGTCTTCTTA AGCAGTGATT TGTGTATGTG  
11151 CTGATATAGC TCAGTATGTC TTTGAAACCA GTTGTCTGGG GCTAGGCCTG  
11201 CAATCAGCTT TTGGCTAAGA GGTCCCAGGA TGGAACAAGT AGTGTGAAAG  
11251 AGGACTGATA CCTTGGCCTC ACACACAGTA CTGCTCTTAG ACTGGGGCAA  
11301 GTGAAACTCC TCACTTCAGA GTGCCCCATT CTAGGCCCCC TCACTCCCAA  
11351 AGGGGTGAGG GATCACTGGG GCCATGGGAA TGTGCTTGTT CAGCTCTCGT  
11401 GGGCTCTCCT TCTGTACCAC GTTCTGGACA TCTGGAGTTC CTTGCCCCAA  
11451 ATCCCTGAGC CCACGTCTGC GTCCGCACAG TCTATTTCTT AAGGTCAGTC  
11501 CATCTCCTCC AGGTGGGAAC GTGCCACCAT TGAAGTGCC CTTGGGCCTG  
11551 AGTGATGGCC AAGGGCTGTG TTGGGGAGTG TTGTGGATGG ATCCTGGCAC  
11601 CGAGGGCTGG GATATCCTCT CAAATGAATG TGAGGTGCCT CCCAGTGCTG  
11651 GAGAGAGCGG GATTCAAGAA GCAGTGGAAG GGAAGAGCCT GGGATATGGG  
11701 GATCAGCTGT CTGTGCCCTG CTGCATTCTG GAATAAAACT CTGAGGGACT  
11751 AAGAATTCTA AATTCAAACC TGAATCAACC AGGTTGTTAC AAAGATAAGT  
11801 TTGTCAGTGC AGGAGGATAC AATATATTTT ACTTAAGTTA CTAGCTCGAT  
11851 TGATCATTTT TAAATTTTTA GCTACATATA GTATGTGGG CTCCATTGTG  
11901 CCTCTTATCC CAGGCCTTGC AGAATTTAGG AATAAGCCTC AATACAGTGT  
11951 TCTAACCCAG TGACTTCCGC CTCGATGTAC AGTAGATTGA ACCTGATCCT  
12001 TTATACTTTA GTGATCATTG GTTGATACCA GTTCAAGTCA GGCTTTCTAG  
12051 AAATCTCATT GTATGTTAGG GGTTTCGATTA GAGTACAGTC ATGCATCACT  
12101 TAATGAATGG CCACAGGATA CATTCTGAGA AACGCATTGA TAGATGATTT  
12151 CATCATTCTG TGAACATCAT AGAGTGTACT TACACATACC AAGATGGCAT  
12201 AGCTACTACA GAGTGGGCT CTGTGGTACA GGCCATTGCT CCAAGGCTGC  
12251 ACATCTCTAC AGGATGGTAC TGTACTGAAT ACTGTAGGCA ATTGGAGCAC  
12301 AGTGGTAAGT ATTTGTGTAT TTAACATAG AAAAGGTATA GTAAAAACAG  
12351 GGTGTTACAG TCTTAAGGCG CCACCATTGT ATTTCCAGTC TCCGTTGACT

FIGURE 2D

12401	GAAACATCAT	TATACAGTAC	ATGAGCACGT	ATCTTTCTCA	CCTGGTACTA
12451	GTGGAAAGCT	AGAAGGCTTA	GAAGTCTACC	TGTAAACATA	GCTTAAGTAA
12501	TAATACAGCC	TTATTTTTTA	ATGATAATAG	CAATAATAGT	GTTCACTTAT
12551	TGAGCATTTT	ACTATGAGTT	ACTTACTAAA	TATATTTTCAT	CGTTAATTTA
12601	CTCTTTGTGT	TATTTGATCT	ATAACATCGT	TTAACAGGGA	AATTACCTAG
12651	TACATAATGT	ACTGTTATCT	ACATTTTATC	TAGATGAGGA	AACTGAGGCA
12701	CAGAGAAATT	AAGTACTTTG	CCTAGGATTA	CCCGTGAAGT	TAAGTGACAG
12751	AATCAATGAA	TCTGGAAGGT	CTGGCTTCAG	ATCTCTGTGT	CTGAGTCACT
12801	CGCATACTTT	ACTACCTCTA	AGGTTTCTAA	TCAGAGGAAT	TTGTATCTGT
12851	ATTCCCTGCT	ACTCTTACCC	TCTATGTGGG	ATTTGGCCTT	TCTCCATTAT
12901	CCCTGTGAAC	TCGCTCTGGG	ACCTTCCTTC	TTGTACTTGG	AACCATCAGA
12951	AAGTGATCTG	AGAACATAGA	AATCTACTGT	GTTGTGAAAC	AGAATTACCT
13001	GGAAGCGGAA	AAAGCCCTCC	TGGCTCAATT	CACATGTCAC	GGCTTATGGT
13051	CGTATCCGGG	GAACATATGA	AACTGGGCAC	TGAGTGCGGA	GTCAGGAAAG
13101	CCCTGTCCAT	CCTCTGGGTT	TCTGGGGAAA	ACGTGGACCC	CTTCATTGTC
13151	ACTTTCTCCT	GTATATTTTT	GTTTTTACTT	TTAGAACTGT	ACAATTACGT
13201	AATAAATAAT	AAAAAGTCGT	TGGAAGGATA	GGTGAAGTTC	AGAAGTGAAA
13251	GTGTTTTGGA	GGAGTCTAAG	CTCCTTCCCA	CCCTCATTGA	CCTTTCCTCT
13301	CTAATAAATA	GAACTGGTCT	AACCAAGGAT	CTGTGGAATG	AGCAGAGTCC
13351	AACGGAGATT	CAGGGATTCT	AATAACCTCT	TGTAGAATCA	CTGGTTTGTT
13401	TACGCCACAA	GAGGAATTA	CCTTTTGACA	TTGGCTTGAA	CAGTGTGTGT
13451	GCAAAGAAAA	ACTTTTGGGA	AAGTTCTGGA	AGTACCAGAT	TGATTTTATA
13501	GGTTTTTTTT	TTTTTTTTTG	GAGGGACATG	GGGGTATTGA	CAGTTGATGT
13551	TAATCAGAAA	TCCTAAATTA	TGTGTATTCC	TGGTATGTG	CAATCAGCCG
13601	GCCACCTGGT	TTTCTCTGG	GCTCTTAATT	TTAGGTGTAT	TCCGAGGAAG
13651	TTTTTCTAAC	TTTTCTGTAA	ACACAGACCA	GGTATATTGC	ATACTTTCAA
13701	TGTTTAACCA	AATCTCTTCA	CTGTTTGCAG	TATTATCTGT	AGGCTCTCAT
13751	GTTTTAAGAC	TTCCCCATGG	TGTTTTTGTA	TTGTATTTTG	CTAACCTATA
13801	AACAATTCTT	TGAACTTAAA	ACAAGATATT	TGGGCAGTAA	CAATAAATTT
13851	TAAAAACATC	AATTCAACTT	TTTTACATTA	GGGCTTGGAC	TATGGAAAAA
13901	GTATTGGGCA	GCATGCCTCA	TACTGAGTTG	TTTAATGAAT	TTAAAAGTAT
13951	AGCCNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
14951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN

FIGURE 2E

Docket No. CL001201DIV  
Application Serial No. TBA  
Inventors: Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEIN...

15501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
15951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
16951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
17551	NNNNNNNGGT	GGAGAGTTCT	GTAGATGTCT	GTTAGGTCTG	CTTGGTCCAG
17601	AGCTGAGTTC	AAGTCCTGGA	TATCCTTGTT	AACCTTTTGT	CTTGTTGATC
17651	TATCTAATAT	TGACAGTGGG	ATGTTAGACT	CGCACACAAT	AATAATGAGA
17701	GACTTTAAGT	CTTTTCTAG	GTCTCTAAGG	ACTTGCTTTA	TGAATCTGGG
17751	TGCTCCTGTA	TTGGGTACAT	ATATGTTTAA	GATAGTTAGC	TCTTCTTGTT
17801	GAATTGATCC	CTTTACCATT	ATGTAGTGGC	CTTCTTTGTC	TCTTTTGATC
17851	TTAGTTGGTT	TAAAGTCTGT	TTTATTAGAG	ACTAGGATTG	CATTCCCTGC
17901	TTTTTTTTTT	CGCTTGGTAG	ATCTTCCTCC	AGCTGTTTAT	TTTGAGCCTA
17951	TGTGCATCTC	TGCACGTGAG	ACGGGTCTCC	TGAATACAGC	ACAGTGACGG
18001	GCCTTGACTG	TTTATCCAAT	TGCCAGTCT	GCGTCTTTTA	ACTGGGGCAT
18051	TTAGCCCACT	TATATTTAAG	GTTAATATTG	TTATGTTTGA	ATTTGATCTG
18101	TCATTATGAT	GTTTGCTGGT	TATTTTGCCC	ATTAATTGAT	GCAGTTTCTT
18151	CCTAGCCTCG	ATGGTCTTTA	CAATTTGGCA	TGTTTTTGCA	GTGGCTGGTA
18201	CCAGTTGTTT	CTTTCCATTT	TACTGCTTC	CTTCAGGAGC	TCTTTTAGGG
18251	CAGGCCTGGT	GGTGACAAAA	TCTCTGAGCA	TTTGCTTGTC	TGTGAAGGAT
18301	TTTATTTCTC	CTTCACTTGT	GAAACTTAGT	TTGGCTGGTT	ATGAGATTCT
18351	GGGTGAAGAA	ATGCTGAATA	TTGGCCCCCA	CTCTCTTCTG	
18401	GCTTGTAGGG	TTTCTGCTGA	GAGATCTGCT	GTTAGTCTGA	TGGGCTTCCC
18451	TTTGTGGGTA	ACCCGACCTT	TCTCTCTGGC	AGCCCTTAAC	ATTTTTTCCT
18501	TCATTCAAC	GTTGGTGAAT	CTGACAATTA	CGTATCTTGG	GATTGCGCTT
18551	CTCGAGGAAT	GTCTTTGTGG	TGTTCTCTGT	ATTCCTGAA	TTTGAATGTT

FIGURE 2F

18601	GACCTGCCTT	GCTAGGTTGG	GGAAGTTCTC	CTGGATAATA	TACTGAAGAG
18651	TGTTTTGTAA	CTTGGTTCCA	TTCTGTCTAT	CACTTTCAGG	TACAACAATC
18701	ATAGCATTGG	TCTTTTCACA	TAGTCGCATA	TTTATTGAAG	CCTTTGTTCA
18751	TTTCTTTTCA	TTCTTTTTTC	TCTAATCTTG	TCTTCTTGCT	TTATTTCATT
18801	AATTTGATCT	TCGATCACTG	ATATCCTTTC	TTCTGCTTGA	TCGAATCGGC
18851	TATTGAAGCT	TGTTTATGCT	TTGTGAAATT	CTTGTAATTT	GGTTTTTCAGC
18901	TCCATCAGGT	CATTTAAGCT	CTTCTCTACA	CTGGTTATTC	TAGTTAGCCA
18951	TTTGTCCAAC	CTTTTCTCAA	GGTTTTTAAGT	TTCTTGCGA	TGGGTCAGAA
19001	CGTGCTGCTT	TAGCTTGGAG	AAGTTTGTTA	TTACCAACCT	TCTGAAGCCT
19051	ACTTCTGTCA	ACTCGTTAAA	CTCATTGTCC	ATCCAGTTT	GTTCTTTTGC
19101	TGGTGAGGAG	TTACGTTCCCT	TTGGAGGAGA	AGAGGCGTTC	TGTTTTTGGGA
19151	ATTTTCAGCC	TTTCTGCTGT	GGTTTCTCCC	CATCTTTGTG	GTTTTATCTA
19201	CCTTTGGTCT	TGCTTTTGGT	TGACGTACAG	ATGGGTTTGT	GTGTGGGTGT
19251	CCTTTTGTGT	GATATTGATC	CTATTCTTTT	GTTTGTTAGT	TTTCTTCTA
19301	ACAGAGGCC	GTCAGCTGCA	GGTCTGTTGG	AGTTGCTGGA	GGTCCACTCT
19351	AGACCTGT	TACCTGGGTA	TCACCAGTGG	AGGCTGCAGA	ACAGCAAATA
19401	TCGCGCCTG	ATCCTTCCTC	TGGAAGCTTC	GTCCAAGAAG	GACACCCACC
19451	TATATGAGGT	GCTGTGCGC	CCCTACTGGG	AGGTGTCTCC	TCCCAGTCAG
19501	GCTACATGGG	GCTCAGGGAC	CCACTTGAGG	AGGCAGTCTG	TCCGTTACTG
19551	GAGTTCAAAT	GCCGAGCTGG	GAGAACCCT	GCTCTCTTCA	GAGCTGTCAG
19601	GCAGGGATGT	TTAAATCTGC	AGAAGCCGTC	TGCTGCCTTT	TGTTTAGATA
19651	TGCCCTGCCC	CCAGAGATGC	AATCTAGAGA	GGCAGTAGGC	CTTGCGGTGG
19701	GCTCCACCCA	GTTCAAGCTT	CCTTGCTGCT	TTGTTTACAC	TGTGAGCATA
19751	GAAGTGCGTA	CTGAAGCCTC	AGCAATGGCG	GGGAGGCGCT	TCCCCTCACC
19801	AAGCTCCAGC	ATCCCAGCTT	GATCTCAGAC	TGCTTGGCTA	GCAGCAAGCA
19851	AGGTCCATG	GCGATGGGAC	CCCCCGAGCC	AGGCACTGGA	GGCAATCACC
19901	TGCTCTGCCA	GTTGCGAAGA	CTGGGAAAAG	CACAGTATTT	GGGCAGAGTA
19951	TACTGTTCTT	CCAGGTACAG	TCACTCACGC	CTTTCCTTGG	CTAGGAAAGG
20001	GAAATCCCCT	GACCCCTTGC	ACTTCTTGGG	TGAGGTGACG	TCCTGCCCTG
20051	CTTTGGCTCA	CCCTCCATGG	GCTGCACCCA	CTGTCCAACC	AGTGCCAATG
20101	AGATGAACCA	GGTACCTCAG	TTGGAAATGC	AGAAATCACC	CATCTTCTGC
20151	ATCGATCTTG	CTGGGAGCTG	TAGACCAGAG	CTGTTCTTAC	TGGGGCATCT
20201	TGGAAGCAAC	TCTGGGTCTG	AGTTTCTGTT	TGTTGCCCTG	ATGTATATCC
20251	CCAGTGCCCTA	GAATGATACT	TGTTACATAG	GAAGTGCTTG	ATCCATGTTT
20301	GCACAAATGA	ATCTTTCTCA	TAATGAGGTT	TCTCTAAACA	AGCTGTTCTC
20351	CCAAAACTT	ACACCCAGCT	TTATGTTGAA	GCATCTCATT	ATACATTGGA
20401	AAGATGAAAT	GTGTAGTGAG	ACTTTGAATC	TTCTTTTGAA	TCTAGAAACA
20451	TTAGCATTTT	TAGACCATT	TATTTTAATA	TTTATGAAAT	TTATGAAATA
20501	ATAAGAAACA	TAGGGCCGGG	CTCAGTAGGCT	TATGCCCTGTA	ATCCCAGCAG
20551	TTTGGGAGGC	CAGGGCTAGT	GGATCATGAG	GTCAGGAATT	TGAGACCAGC
20601	TTGGCCAACA	TGGTGAAACC	CCACTTCTAC	TAAAAATATA	AAAATTAGCT
20651	GGGCGTGGTG	GTGCATGCC	GTAATGCCAG	CTCCTGGAGA	GGCTGAGGCA
20701	GGAGAATCAT	TTGAACCTGG	GAGGCGGAGT	TTGCAGTGAG	CTGAGATCGT
20751	GCCATTGCAC	TCCAGCCTGG	GCAACATTGC	GAGACTCCAT	CTCAAAAAACA
20801	AAAACAAAAA	CAAAAAAAT	GTGTGACCTA	AATTAGGCTT	ATAGATGAAC
20851	CATTGCAGTC	ATGATTAATT	CCGCCATTGT	TTGCCTTGTG	ATCTTTGGTG
20901	CCATGTCTGT	ACATATTTCA	TGATTTCTGT	GTTTTTACGG	TTTCCATTTC
20951	AGATCTCCCT	TGAGTTTAGA	AATCTGGCTG	AGAAATACCA	AACAGTGATT
21001	GCCGACATTT	GCCGGAGAAT	GGGCATTGGG	ATGGCAGAGT	TTTTTGATAA
21051	GCATGTGACC	TCTGAACAGG	AGTGGGACAA	GGTTAGTCTC	ATAAAACAGT
21101	GTCTGTGTGT	GATGTATTAG	ACAGAGCTGG	CAGTCTCAT	AGTGAAGCTC
21151	AGAACAAGAA	AAGTTGTCCA	GTATTTTCAG	CCCCTCTGGT	TTTACAATTC
21201	ATCTGTTTAG	GTTGAATGTC	TCATCATAAA	CAGTTTATTC	CAGAGTTAAT
21251	TCCAAACCAG	CAGCTATGTA	GGATATCAGC	CAGGCTAGGA	GTAGGGTACT
21301	GGAGAGAAGT	GCTTATCTAG	ACAAAGGGAT	GTAATTGACC	ATGAAGATTA
21351	AAACTACACA	TCAAAACATA	AGGTAGGGTT	AGGAGTCTTG	CCTATTTTTC
21401	ATAGGAATGG	TGTTTGTGAG	ACTTACTCAT	CACTTCTGTG	GAAGTAAAGA
21451	CATTTTATTT	ATTTATTTTA	AAGCCAGTCA	GATTTAGCAG	GCAGAGACAT
21501	TTCAGACATC	TAAAGTGTTG	ATGTATTTCA	TACCTTTAAC	TGTGCTTAAA
21551	TTAGGATCTC	CGAAAAGATG	CTGCTACATG	GTCACACG	TAGTGAGGT
21601	CCAAGGTCTT	GGGCCCTCTTA	ATTTTTCAAA	CCTCAAACT	TGACAGCAGT
21651	TATCTTTGGA	ACTGCTGATT	TGTGCTTCTT	AAGTTAACAG	CATACAATGA

FIGURE 2G

21701 CTGCTAGAAA TCAATTTCTG CATTTAAGGT GAAGTTAGCC GGGTACTATG  
21751 GTTTACCTGT AATCTCAGCA CTTTGGGAGG CTGAGGTGGG AGGATCATT  
21801 GAGCCCAGGA GTTAGACACA AGCCTAAGCA ACATAGCGAG ACCCGTCTT  
21851 TCAAAAAATT AAAAAATGAG CAGGGAATTG GTGGCATGTG CCTGTGGTCC  
21901 CCAGCTACTC TGGAGGCTGA GGTGTGGGAG GATTGCTTGA GCCCAAGAGT  
21951 TGAAGGTTGC AGTGAGCCAT GATTGTGCCA CTGCACTCCA ACGTGGGTGA  
22001 CAGAGCAAGA CACCTACTGA AAGAAAATAA AGTTGAAGTT AAAACTTCTG  
22051 GCCAAGAACC AGCACTGGTT ATGATAGTAA CTCATTTTCT GTTGTGCAGA  
22101 TTTATTCAAG AAACCTAATT TTAGGTTGTT GAATAGAAGT TTTGATCAGA  
22151 TAAAATTGAA TTAATAAAAA TTTTTTTGA GACAGGGTCT TGCTGTTATC  
22201 CAGGCTGGTG TGTAGTGGTG TGATCACGGC TCCCCGAGC CTCAACCTCC  
22251 TGGGCTCAGG TGATCCTCCC ACCTCAGCCT ACCGAGTAGC TGTAACACAA  
22301 GTGCATGACA CCATACCAGG CTCATTTTGT TACATTTTTT GTAGAGAGAG  
22351 GGTTTTGCCA TGTTGCCCAG GCTAGTCTCA AACTCCTGGC ATCAAACAGT  
22401 CCTCCCACTC TGGCCTCTCA AATGTTGGGA TTACAGGCAT GACCAGCCAA  
22451 TTATTTCAGG GAGTTATTTT TTTTCTCTA CTTTGGGGGA AGATGAATTA  
22501 TATAAGTCTC CATTTTAGGA GTATTTCTAC CAAAAGAACT ATTATCTTCA  
22551 AATATATTTT TGGATAGTAC TATAGATATA CTAATTTTTT TTTAAATTTT  
22601 TAGTAATTTT TTTGAAGATT TTGTATAGCT GTCCAAAGCC AATTTCTGTC  
22651 TACCTAATTT CAGCAAGATT TCACTCTTTT CATGTTACTT TTGTCCAGA  
22701 ACAAATTTCA AGTGCTTTCT CTTACCTGT GCATTCTTCC CCCTGATTAG  
22751 TCTCTGGCTT TGTATTACTT TCAGTCAGAG ACGACTTTTT TTTTGTGAGA  
22801 CAGGGTCTCA CTCTGTCAAC CAGACTGGAA TGCAGTGGCA CAGACAAGGC  
22851 AGCCTTGACC TTCTGGGCTC AAGCAATCTT CCTTGCCCTC AGCCTCCTGA  
22901 GTAACCTGGA CCACAGGCAC GTTGCCACCA TGCCCTGGCTA ATTTATTTTA  
22951 ATTTTATTTA TTTTGTAGAC AGGGTATTGC TCTGTCACCC AGGCTGGAGT  
23001 GTAGTGGCAT GATCAAGGCT CACTGCAGCC TTCACCTCCT GTGCTCAAGC  
23051 AGTCTCTCA CCTCAGCCTC CCCATTAGCT GGGACTATAG GTCCACACCA  
23101 CTACACCAGG CTAATTTTGT TAATTTTGTG GTAGAGACAG GGTTCATCG  
23151 TGTTGCCTAG GCTGGTCTTG AGCTCCTGGG CTCAGCGGAT TCACCTGCCT  
23201 TAGCCTCCCA GGTGTGAGCC ACTACACTCA GCCTTTTAAA ATTTTGTACA  
23251 GAGATGAGT CTTGCTTTGT TGGCCAGGCT GGTCTAAAAC TCTTGGGCTC  
23301 AAGCAGTCCC CTCTCCACAG CCTCCCAGAA TTCCGGGATT ACAGGCGTGA  
23351 ACTTCGGTCA TTTCTTAAC TTTACCCCTC CTAATGACAC TCCAGAGCTT  
23401 ACCTTCTTTA CTTTGTCTTC TTAAGTTAAC TAATAGACAA TTATTGTATG  
23451 TGGATATTGC ATTAAGTTGT CTTAGGATAC CCTTTTCAGA GGAGGACAGC  
23501 TTTTGACAAA TTGCTGTGCG GGAAAAAAA AGTATTTGGC AATTAAGAGT  
23551 TGCATTTACT GAAATCTCTG TTGAGAGAGG GGAAGTTACG TTGTCTCTAA  
23601 AAGAAAAAAT AAAAAAGAAA GGGGAAGTTT TAGCAAAGTT GTTAAAGCCT  
23651 GACACTTAAG TCATACTACC TAGTTTGTGA CTCTTAGCCC CTGCCACAGA  
23701 CACGGCAGCC CCTTGAACCT TCCTGGGTTT AAGCGAGCCT CCTACTTCAG  
23751 CCCCCTGAGT AACTGGGACC ACTGGCCTGT GTCAGTGTGC CTGGCTAATT  
23801 TTTTTTTTTT CCTCACATGG GCAATGTTGG GCAAGTTAAA TCGACTTCTT  
23851 TGTGCCTCAG TTTCTCTATC TGAAATGGAG ATCATACTGC TATGTACCTG  
23901 ATACAATGTT TGTGAGGATT GAATGTGCAG AGTTCTTTTT TTCTGTTGTT  
23951 GTTGTTTTGA GACGGAGTCT CACTCTGNNN NNNNNNNNNN NNNNNNNNNN  
24001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN  
24051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN TCTCGTGATC  
24101 CGCCCGTCTC AGCTTCCCAA AGTGCTGGGA TTACAGGCAT GAGCCATCGT  
24151 GCCCGGCTGA ATGTGCAGAG TTCTTAAAC CGTGTCAGA ACATAAAATA  
24201 GTTATTTGTT CTTTCATATA ATGATGATTT TGAGGGCCTG CGGATCTTGA  
24251 CATGTTATCA GATTGGTCAA AAAAAGATTA AACCATAGTT GGTATTGTCC  
24301 TAGTTCCTGT TACCAGAATA TTCCATCTTT CATCGTTGCC TTCTCTCATA  
24351 GTTTTATGTA TCAAAAAGTT TATTGTAAAG CTAGGCCGGG CACGGTGTCT  
24401 TGGGCTGGTA ATCCCAGCAC TTTGGGAGGC CAAGGCTGGC AGATCAGTTG  
24451 AGGTCAAGGAG TTCGAGACCA GCGTGGCCAA CATGGTGAAA CCCCGTCTCT  
24501 ACTAAAAATA AAAAATTAGC TGGATGTGGT GGTGGGTGCT TTAATTCCAG  
24551 CTACTCAGGA AGCTGAGGCA GGAGAATCAC TTGAACCCAA GAGGCAGAGG  
24601 TTGCAGTGAG TTGAGATTGT GCCACTGCAC TCCAGCCCAG GGGACAAAGT  
24651 GAGACTTGAT CTCAAAAAAA AAAAAAATAA AAAGTTATTG TAAAGCTAGA  
24701 CACGGTGGTA TTTGCCTACA ATCCCAGCTG TTCGGGAAGC TGAGGCAGAA  
24751 AGATTGCTTG GGTCCAGTAG TTTGAGTCTA ACGTGGGCAA ATATATGAGA

FIGURE 2H

Docket No. CL001201DIV  
Application Serial No. TBA  
Inventors: Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEIN...

24801	CTCCATCTCA	AAAAAAAAAA	TAAAAAATAA	AAATAAAAAA	ATGTTTACTA
24851	GTTTTTTTCA	GTAGCCTTTT	ATTATAGTAG	CAGTACATGT	GTATTGTAGA
24901	AATTTGGAAA	ATACAAGTGA	AAAATAAAAA	CATCAAAATC	CCGTCAGCCA
24951	GAGACTGCTG	TGAAATGTTT	TGAGCACATC	CTTCTTGAAT	GTTTTTTAAA
25001	TCCTGGTATG	TATATTTGTA	TTTTAAAATC	AAAATGCATT	CTTACCCATT
25051	CTCTTTTGAA	CCTGCTTTTT	TGTAGCTAAT	GATCTCTAGT	GTGTCCATTT
25101	CAGTAAAAAT	TCCATTATTA	AAGTGCTTTA	AAAATCGTCT	CTTACAGTAC
25151	TGCCACTATG	TTGCTGGGCT	GGTCGGAATT	GGCCTTTCCC	GTCTTTTCTC
25201	AGCCTCAGAG	TTTGAAGACC	CCTTAGTTGG	TGAAGATACA	GAACGTGCCA
25251	ACTCTATGGG	CCTGTTTTCTG	CAGAAAACAA	ACATCATCCG	TGACTATCTG
25301	GAAGACCAGC	AAGGAGGAAG	AGAGTTCTGG	CCTCAAGAGG	TAACAGATTC
25351	AGGGTATTTT	GGGGGAAAAT	AACTTTAGAC	ATTCTCTGAA	AAATCCTTTA
25401	ACTCTTGTGG	TTGCGGGTGA	CAGAAAAACA	AGCCAGGCCT	CCCCCAGGCA
25451	GCATAAGGGG	ATGTGGAAAA	TAGGATAGAT	TGACATGAGT	TTGCTTCAGG
25501	TAGACTGGCT	GACTCCCAGG	ATTCACACCA	CGTAATCAGT	ATATTCAAGC
25551	CTTGCTGTCC	TTGATTTCTT	TCAGACGGTC	TTTCTCCAAG	TGGTGGATAT
25601	GGTAACAACC	CACGTGCACT	AGCTTAACAA	AAAGTTCTTA	GGAATGGCTT
25651	TGTTCGGCCT	GGCGCAGTGG	CTCATGCCTG	TAATCCCAAC	AGTTTGAGAG
25701	GCCAAGGTGG	CGCGATCACC	TGAGGCCAGG	AGTTCGAGAC	CAGCCTGGCC
25751	AACATAGTGA	AACCCCGTGT	TTACTAAAAA	ATACAAAAAT	TAGCCGGGCG
25801	TGGTGGAAG	GGCTTGTAAT	CCCAGCTACC	TGGGAGGCTG	AGGCAGGAGA
25851	ATCGCTTGAA	CCCAGGAAGC	AGAGATTGCG	GTGAGCTCAG	ATTGTGCCAC
25901	TGCACTCCAG	CCTGGGCGAC	AGAGTGAGAC	TCCCTCTCAA	AAGAAGAGGA
25951	AGGGCTTGGT	TCTTCTGCTC	AGCCCTGAAT	CAGTTACTGT	TGCTACACAG
26001	CTGAGTTCTC	TGGCCTCACC	TGGATTACGT	CTACACAGTA	CACACAGAAT
26051	GGATTTCCCC	CAAAGAAAGA	ATTCTGCGGC	AGGAAGGGGA	AAGGGATGGC
26101	AGGTAGACAA	AAACTCCAGG	TGTCTGTAAT	AAGGGACAGG	GTCGATCTTT
26151	AATTAAAACA	TGGACAGGGA	ACAGAAAGCT	TTTGATACTG	ATTTTGTTCa
26201	GAAGGAAAGT	AGAAAATTTT	ATGACTGTTC	CCTGAATTTA	TTCCAGCATT
26251	TACCTTTTGC	TTTCCATAAA	AGTGTTTCCT	GCAGCCAAGT	ACTTTAAAGT
26301	TTTAAAAAGA	CGGGTGAGGC	TAAGTGTGGT	GTCTCATACT	TATAATCCCA
26351	GTGCTGAGGC	CAGGAGTTCA	AGACCAGCCT	GAGCAACACA	GCAAGATACC
26401	ATCTCTATAA	AAAATTGTTA	GAAAATGATT	CTGCTGAAAG	AGCAAAAATA
26451	AAAATTAAAG	AAAGTAGAAA	AAATAAAACT	AAATTTAAAA	GATTAAGTGG
26501	GCATGTTGGC	ATGCACCTGT	ATTCTAGGTT	ATTCGGGAGG	CTAAGGCACA
26551	AGGATCCCTT	GAGCGCAGGA	GCTCAAGGTT	GGATTGAGTT	GTAATCACAC
26601	CACGTGCACTC	CAGCCTCGGT	GGCACAATGA	AACTGTCTCA	AGAAAAAATA
26651	AAAGTGACAG	AGGGAAACAA	TATTTGCAAT	TCATAGAGCA	GATACAGGGT
26701	TCATATTCCCT	AATATTAAAA	AAAACCTCTA	AAAGTTAAGA	AAAAGGCCAA
26751	CTGCCCCACA	GAAAAATGGG	CAAGGAGATA	AGAACAAGAT	TGTTTCACAGG
26801	AAGAGACACA	CAGATGATTA	TTAAAAATCT	GAAAAGATGC	TGAGTCTTAC
26851	TCCTAAGAAA	AATTCACATT	TAAACTACTC	TGGGGGCTGG	GCAAGGTGGC
26901	TCACGCCTGT	AATCTCAACA	CTGGGAGACC	AAGGCAGGAA	GATCACTGAA
26951	GCCAGGGTAT	CGAGACCAGC	CTGGACAACG	TAGTGAGACC	TTATCTCTTA
27001	AAACAAAACA	AAACAAAACA	AAACAAAAAA	AACAGTAAAA	ATTGGCCGGG
27051	CACAGTGACT	CCTGCCTATA	ATCCCAGCAC	TTTGGGAAGC	CCAGGTGAGT
27101	GGATCACTTG	AGGTCAGGTG	TTTGAGAACA	GCCTGGCCAA	CATGGCAAAA
27151	TTCCGTCTCT	ACTAAAATTA	CAAAAATTAG	CCAAGTGTGG	TGGCATACGC
27201	TGGTAGGGCC	AGCTACTTGG	GAGGCTGATG	TGAGACTCCA	TTTAAAAAAA
27251	AAAAATCAAA	AATTAGCTGG	GTATAGTGGC	ACACCCCTAT	AGTTCTCGCT
27301	CCTTGGGAGG	TTGAGGCAGG	AGGATTGCCT	GAGCCCAGGA	GTTCAAGGCT
27351	GCAGTGAACC	ATGATCACAC	CACGTGCATT	TAGCAGCCTG	GGAGACAGAG
27401	CAAAACCCTT	GTCTCAAAAC	AAACAAAACA	CAACAAAAAC	AAAAAACACT
27451	TCCCTCAGCT	CAGACATGGC	CTTTTAAGTT	TCCTAGGTGA	CTCGTGTGCA
27501	GCCAGGGTTG	AGAAACCACT	CTTGTCTTAC	CCCTCTTTTG	CAGACACAGG
27551	GCTCAGAGAA	GGGAAGGGGA	TTGTCTGGGG	ATGTATAGTG	AGGCAGTGGC
27601	TGCCTTGGA	GTGGAGTCTC	AGTCTCCCGG	CTCCTAGGCC	AGCCCCTGAC
27651	CACTGTTCCA	TTGTCTCCCA	GACAGAACAT	CAGCCACGGG	CATGTGATGC
27701	ATGAGCGTGA	TTCACACCAT	CTTGACACAC	CAGGAGCAGA	GCCCTGCTCT
27751	TCTCATTAC	TTACTTTATC	TGTAATAATAG	CATCATTTCT	ACCACACGGT
27801	GGTGGTGTGA	ATAAAATGAG	ATGAACTTCT	AGCATAGAGT	GCTTAGTAAA
27851	GGTTCTGGAC	ATTTCTGATG	AGTTGAATCA	TGCCAAATGT	GGTCTTAGGT

FIGURE 21



Docket No. CL001201DIV  
Application Serial No. TBA  
Inventors: Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEIN...

27901	GATTGGCTTC	TTTTGCTAGC	ATGTTTTTCAG	GGCTCCTCCA	TGCTGGGGCA
27951	TTGCATCACT	GCTTTATTCC	TTTTTATCGC	CTAGTATTAT	TCCACTGTGT
28001	GGATAGACCA	CATTTATCCA	TTCATCAGTT	GGAGGATATT	TGGGTTCTTC
28051	CCATTTTTTT	TGCTATGGT	GAATAGTACT	GTGTACATTT	GCATATAAGG
28101	TTTTGTGTAG	ATGTGTGTTT	TCCTTTTTCT	TGGGTCTATG	CTGAGAAGTG
28151	GAATTGCTGG	TTCATACAGC	AGCTCGAACC	TTGTGAGGAG	CTGCCAGACG
28201	CTTTTCCAAG	GTGCTCCAC	CATTTTACAT	TCCCGTCAGC	AGTGTGAGAG
28251	TCCCAGTTTC	ACCAGCACTT	GTTGTTATCT	CTTTTTAACT	GTATGTATAT
28301	ATACTTAACA	TTTTATTAT	AATAAATGTA	CATAATAGAG	AATTTGCCAT
28351	TTTAACTATT	TTAAGTCTA	TTATTCAGTG	GCATTAAAGTA	CATTAATGAT
28401	GTATATAAAC	CATCAACACT	ATGTTTCCAG	AACTTTCGCT	AGCTTCAGAG
28451	AATCCTCTAA	ATAATATCAT	TAAAAATCAT	CAAGCCGAAT	CCCCTGTTA
28501	GAATTAAAGG	TTTTATTTC	CTTTCAAGTT	ATCAGGATCC	AGGGAGGTGT
28551	AATACACCTTA	GAGGATAGAC	TCAGCTCATT	TCCCAGCTAT	GCCTTTCAGC
28601	AGCATTCTTA	CCAGAGTAGG	AATATAATGT	TAGTCATTAT	TTAGAGGCCT
28651	GGCCATCTTG	AGAAGGTTTA	CTGTTTAGTC	TGCAGTACAA	TTATAACTGT
28701	TTTTGTATAT	TGGGTTATTT	TTTTCAGAAG	TAGGCCAGTA	GCTCTAACAG
28751	GAGCCTCTTT	AGCCTGAATT	CGTCCAAGTA	GTGCAGTGTT	GCACTAGTTG
28801	TCCCTCGGGA	CATGCTCCCC	AATACGTAAC	TCACTTCCAG	GTTGCAACTG
28851	GACACTTACT	GGTAGTCAGA	AATAGCTATT	GCATGGAGCT	TAAAAAGAAC
28901	TTGATCTTCG	TGAAAAGATGA	GTCTGCAGCT	AAGAGACTTT	ACTGTATATC
28951	ATAGTGTTTT	TTTTTGTTTT	GTTTTGTTTT	TGTTTTTGTTG	ACGGAGTCTC
29001	ACTCTTTCAC	CCAGGCTGGA	GTGCAATGGC	GAGATCTTGA	CTCACTGCAA
29051	CCTCCGCCCC	CTAGGTTCAA	GCAATTCTTC	TGTCTCACCC	TCCTGAGTAG
29101	CTGGGATTAC	AGGCGCCTGC	CACCGTACCC	GGCTAGTTTT	TGTATTTTTA
29151	GTAGACACAG	GGTTTCACCA	CCTTGGCCAG	GCTGGTCTTG	AACTCCTGAC
29201	CTCGTGATCC	ACCCTCCTCG	GCCTCCCAA	GTGCTGGGAT	TACAGGCGTG
29251	AGCCACGGCG	CCCAGCCTGT	ATCATAGTTC	TTATGCACAA	AGACCCTTTA
29301	ATATTGTTTG	TAAATTCTCC	CCTATGCACA	CGCTGACCTG	TTCTTTAATC
29351	TTCTTATCTG	TCTAGGTTTG	GAGCAGGTAT	GTTAAGAAAGT	TAGGGGATTT
29401	TGCTAAGCCG	GAGAATATTG	ACTTGGCCGT	GCAGTGCCTG	AATGAACCTA
29451	TAACCAATGC	ACTGCACCAC	ATCCCAGATG	TCATCACCTA	CCTTTCGAGA
29501	CTCAGAAACC	AGAGTGTTGT	TAACCTCTGT	GCTATTCCAC	AGGTAGGGAA
29551	CGGGGCTCCT	CTGGGTGGAT	ACGGGGCTAA	AGGGAGTGGG	GTAGGAGTAA
29601	GGGTGGATTT	TGCTGTGCTA	TATTCAAGGA	TATGATTCCT	TAAAAAGACG
29651	ATGACTCCAG	TTTATTACGC	TGGGAGTTTC	ATAGCACCCG	CCTTTGCTTC
29701	CAGCCACCAA	ACTCAGCTCA	GCCTTGAGGT	TAAGCCTGCT	CCTTTTCAGA
29751	ACCTTCTTTC	CGGATTTACT	ATTTTCTACA	GCTATCCTAA	ACTAGTTAGG
29801	TTCTTTCTCT	CACAGTTAAG	TCAAGGTCTT	TGGCTTAGAT	TTATGGGGAG
29851	TGCTGGGTAA	AACCTGGGTG	AAGCTGTTAT	CATTAAAAAG	TCTTCATTAA
29901	GCACCTAATT	ACTGCTGTCC	TTTTCTCTAGA	CCCGGCATAA	AAAGAACCTG
29951	GTCCGGTAGA	CCTAGCCTCT	CAGTATGCTA	GGAACCTTACA	CTTTTTAGTT
30001	GCCTTTACCA	AGTATTGCAG	ATACTACTGC	AAATAAGTGA	AGAAAGTAAC
30051	AGCATTTAAC	TGATTTGGGA	ACTTGGTTTG	ATCTTGTTCT	AATGACCCAC
30101	TTCGAATGGT	GGTTGAAAGT	AAAATCTGTA	TCGCCGTCTT	ATGTTTCCAT
30151	TTACCTAGAA	ATACTTTACC	TTTGAGCACA	GGAAATTAAT	CCCCTTCTGG
30201	TTGTTCTCCC	CCTGGCATTG	GTTTTAAATA	TATAATGATT	ATGTTTGTTG
30251	TAGGAAAAAT	AGAAAAACAA	CTACAATAGA	AAATCTCTCC	CATATATTAT
30301	TTTGAAATAC	ATATTTCCGA	TCCGATAATC	CATTGCTCTA	GCATGGAAAA
30351	TGTTGGATTT	ACTTGTGTTT	GCTTTTTTCCA	AATAAAATGG	AACTTTTGTG
30401	GCTACATTAT	AGAATTGTTT	TAGACTGCTT	AATTCTGTGT	GTTGTTGAGA
30451	AAGGGAGGAG	TGGGGAAGGT	AAAAATCTTG	ACATACTTTC	TTCGTGGGTA
30501	TTTTTTCTTG	AGCGATTCCA	TCTTAGTTGA	TTAGCAGTTA	GCAATTGCC
30551	ATTCAACAGA	AGGTTTTCTT	ACCTTTTTGT	GATAATGATA	GCTAACGACA
30601	TCATTTCTTC	TTTTTTCCCT	CTCTTCTTGT	TGTCTCTAGG	TGATGGCCAT
30651	TGCCACTTTG	GCTGCCTGTT	ATAATAACCA	GCAGGTGTTT	AAAGGGGCAG
30701	TGAAGATTCG	GAAAGGGCAA	GCAGTGACCC	TGATGATGGA	TGCCACCAAT
30751	ATGCCAGCTG	TCAAAGCCAT	CATATATCAG	TATATGGAAG	AGGTGGGTTT
30801	TTATTTAACT	ACTTGGATAA	TTTGTAGCTA	CTTTTATGAT	TTAGTAATGT
30851	CACTGTTTAA	CCAGGTTTGG	ATATTAGATG	ATCCTAACAA	TTCACTATCC
30901	TGTGGCCTAA	AGAGACAGGA	ATTGATATCC	TTTATAAGGA	AAAAAGTCTA
30951	TTACACAGGAG	CCGAGCAGAT	TGCTCACTGC	TGTGTAGTAC	CCTGGTGAGA

FIGURE 2J

Docket No. CL001201DIV  
Application Serial No. TBA  
Inventors: Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEIN...

31001 GGAGATAAAT GGAGCAAGGC TGTAGGTTGG AGCCCCTCAG TAGAATCATA  
31051 GATTTTGAGC TGCAAGATGA TGCAGGAGGC CAACCAAGCT TCTTGTGCT  
31101 GGTGAGGAAT GTGAGGTTGA AGCTTGTCTG TGCTGATGCA GTGCGTGATT  
31151 GAGTGGATCT CTGGCTCCCC TCCATGTGTC CTGACACCCA GTCTGGTACT  
31201 TTCATTATGC CACAGGCCTC AATTGAAAAA TCACAGTAGG GAATTTAGGC  
31251 CAAGGAAAGC CATCAAGTTG CAATTATTTT CTAAATTTTC TTTGGAAAAT  
31301 TTCATTTCAA ATACCAAAAC CATCCTATAA AAAGAAAAC TACCTTCTTA  
31351 GGTCAAATCT CTAATATTTG ACTAGGTTCA AAAAGTTTAT TTCTGGCCAG  
31401 GCACAGTAGC TTAATCCTGA AATCCCAGCA CTTTGGGAGA CCAAGGTGGG  
31451 AGGATCACTT GAGGCCAGGA ATTCAAGACC AGCCCGGGCG ACATAGCAAG  
31501 ACCCCATTTT TACAAAAAAT TTAAAAATG TCATGGTGGT GCACGCCTGT  
31551 GGTCCCAGCT ACTCAGGAGG CTGAGGCAGG TGGATCACAT GAGCCTGAGA  
31601 GGTGAGACTT ACAGTAAGCT GTGTGATTTT ATCATTCAC TCTAGCCTGG  
31651 GTGATAGAGT GAGACTTTGT CTCAAAAAAA AAAAAAATAA AAAAAAGTCTT  
31701 AGAGACCAGA AGTCTCTGTA ATCTCTAATA ATCTCTAGGC CCTAGAGCAG  
31751 TGGTTTGTA ATGGAGGTGA TTTGCTCCCC TCCCCCAGA GGACATTGGA  
31801 CAATGTCTGG AGACATTTTT GATTGTCTTA ACCGGCAGGA ATCGGGTGCT  
31851 ACTGGCATCT GGTGAGTAGA GGCCAGGAT GATGCTGTGA TCCTCAGGTG  
31901 TGATCCTGTT GAGAATGAAA CACTGTAGAC TTTATGAAA CATAACAAGC  
31951 CCTCATCATT TTTCTTTTGC CTGAGCTCCC TCCCCAGAGG TTACCTCTGT  
32001 TCATGGTTTT GTGCATCCGT CTAGTCCCCC TGTTACCGCT TTACAGGAAT  
32051 ATGGTTTGCA ACAGTGTTTT CATCTAAATA GAATTATACA AAATAGCGAT  
32101 TTCTGATTTT TCTTGCATAT TGCACATTCT TCTTATACCT CCTCCCTACC  
32151 TTTATCTGAC ACAGAAATGC TGTATGTCCA GAACCTCTAT CAGAGGCACC  
32201 TATGGAAGTC TAAGGGAAGA CCACATCGCT TTTAAAAACC CTAAATTTT  
32251 GTAGTCACTA GATGAAAATA TTCAGCCAGT GACCCAAAAA ATTGCTACCA  
32301 ATGAGACTCT CCATTTTGCC ATGTAGCCAG AACTTACTTT GATCTATGTG  
32351 CCTGGGGTAG TGACCAAGTA GGTGGGTAGG AGTAATCTCA GGGAAACTTG  
32401 AGGCCCCAGC CTCATGGCTA GGGTCATAAT TTGAACCCAG GTCTGTCTGA  
32451 CATCAGAATC CATGATGTTA ACCCCAATTC TAAGGGGTTC AACTACCTTT  
32501 TCTAAATGGA ATCCTGCTAT ATTAAGCACT ATTTATTCAT TTTATATAAA  
32551 CTAGAAACAT TTTATGTAGT AAGTAGTTGA GAGTGTTTTG GTTTTGCACT  
32601 TTGATCACTA GTTTTAGAAA CCAGTTTTTA AACACTTTGT GGCCAAATCC  
32651 ATTACTATAT TAAAAATCAG ATTTATTTGG TTTTTCCTTA ACTATTGGGA  
32701 TTAATCCTG GTTGTAATTC ATAGTTTGAG GCGAGGGTG GGCAGTCTAC  
32751 ATTTGGCTGA GCCCTGTTTT TGTGAATAAA TGTTATCAGA ACACAGCCAC  
32801 ACCCATTTGC TTCTATGTCT TCTGTGGCTG CTTTTCGAAT GTGACGGCCG  
32851 AGTTGAGGAG CTGCAACAGG CGATGACTTG TAAAGCTGAA AATATTTTTT  
32901 GGCCCTTGAA TAAGAGGTTG GCTGACTTCT GACTTAGGGC ATCAGTTGTT  
32951 CTGTTATCCC AGTAAAACCT AAGGCATTAG GGGAGAAATG TTAATATTAA  
33001 TACTTAAGTT GATTTGATTT AGGGAAATCT TTGAAGATTT CTAAGTCTTA  
33051 AGCAGTAGAA CCTGTTAATG GTTTTAGTTT CAGCAGTAAG GACATTTTAC  
33101 AAGTAAAGTT TTAATGAAA ACATTTTGTA TGAAGCCACA AGTCGTCTGG  
33151 CCTCTTGCTG GTGTCCAGAT ATTAACACTG ATCCTATTTT TCCTTGCTGA  
33201 CCAAGTCTGT CCTTTGTAGT AAGAAAGGAA GAAACGTTGA CTCTGTCCGA  
33251 TCTCTGGACT TAGTGTTGTA GCGAGCATGC ACCTGGAAGG GACTTGCCAG  
33301 AGGACCTCCT CATGCTTCTC CAGTGCTTAG TGGGGGCTTG GAGTGCAGCC  
33351 CCAGGTCTTC ACGAGCAGTT GGCCACACTG CAGGGCCCTC ACCCACTCT  
33401 GGAGCAGCCT CTGCTTCAAA CCAGCCTGGA TGCTTGTCAG CTGGGGAGAA  
33451 GATCAACCTG CTATTTTGGG ATAGAAATAA ATGCTCAGCC AAACGGCCAG  
33501 AAACCCCAT TCCCCTCTCT GCCAAAGTGA ATTCCTTGGC AGGGAGAAGC  
33551 TTGTTCTGTT CTCTGCACAC TTCTGTGCC CTCCTGTGGT TAAGTCAGAG  
33601 AATCATCCGG CTCTTTGAGC CCCAGGTGCC TAGCTGCTCA AGGATGGTCC  
33651 CCAGCCAGCA GCTGCCAGGA ATCACCTGGG AGCCCATTA GACATCCAGC  
33701 CCCCACCCAA ACCTATCGAA TCAGAATCTG CCTTTTTTTC CCAAATGATG  
33751 TTTTCTGCTT AATGGAAGTT TAGATGTTCA TAGACAAGAG TTTTAAATGA  
33801 TGATCAAGCT GATTCCATAT TCGCAGTTGT AAGTAGAACT GCTGAGACGT  
33851 GGAAGTACCA CATGGACTCA CAGAGGAGCT GCTGTATGTA GCACAGCATT  
33901 GCACAAGAGC TTATTTTCAGT CTAGTAAACA TTTATAGGAG CCTGTGTCTAT  
33951 TTAATCATCA AGCCTCGCAC TGTGGCTCAC ACCTGTAATC CCAAACTTTT  
34001 GGGAGGCTGA GGCAGGCAGA TCACTTGAGG TAAGGAGTTC GAGACCAGCC  
34051 TGGCCAATAT GGCAAAACCC TGTCTCTACT AAAAATACAA CATTTAGCCA

FIGURE 2K

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34101 GGTGTGGTGG TGCACACTTG TCATCCCAGC TATTCCGGAG CCTGAGACAT
34151 GAGCATCGCT TGAACCTCGG AGGTGGAGGT TGAGTGAGC TGAGATGGCA
34201 CCACTGCACT CCAGCCTGGG CAACAGGGTG AAGGCCCTTT CTCAAACCTCC
34251 TCAAGTATTT GGCTTCAACT TTATGCCGGG CATGTAGATG AAAAGTCGGC
34301 TATGACCTGT CCTTGACAAG CAGATGTAAC TCCTTGATTG AGGCTAGTAG
34351 GTTTTTAAGA CCTGAATAAT TGAGTTTGCA GAAACCTACT GTGTGCCTTC
34401 AGGTAAATGG AGAGTGGGGT TTGGTCTAGC AACGAAGCAT CTAGAAGGTC
34451 TCTTTGGCCT TACCGGCTCT GTTTTAGGTA AGTCCACGTC TGAGTACCAG
34501 TGACTGCAGC TCTTCCAGTT GTGCTGTCAT GTTTATATGT TAGAAATGAT
34551 CATCAAAGGA CTCAAAGATT TTGCCACTAA TTGTATTACC GGGGACTGTC
34601 ACAACCAAGA TTTCTCTTAA TTTATTCACT TTACTTATCT CCTGGAAGGG
34651 CATATTGAAG TGCTCTTGGA GTTCTCTAAA AGGGTTTTTG TTGGTTGTGT
34701 ATATTCACCT GGGTGCCAGC GATTGATTCC AAATAAGTAA ATCTTTTTTC
34751 CCAAAAGGAT GTAAGATGGC TTATGGTTAT AAGTACAACA GGCTAACAAA
34801 GTACAAGTAG ATGAGAAAGT AAAATGAAGA AATAAAGTCA TAGGAGCCAC
34851 AGAATTAACC CAGGAATGAA TAAGTGTGTA GTTTGGTGCT GATGTTATCA
34901 TCCTTTATTT GTACATTGCT TGTACAGTTG CTCTGAGAAG GTAAGTCTTA
34951 AATTTTCAAA AGTGAAATGT CACCGAGCAT GGTGGCTGAT GCCTCTAATC
35001 TCAGCAGCTTT GGGAGGCTGA GGCAGGCGGA TCACTTGAGG TCAGGAGTTC
35051 GAAACCAAGC TGACTTATGT GATGAAACCC TGCTCTACT AAAAAAAAAA
35101 AAAAAAAAAA AAAAAAAAAA AAAAATCCAA AAGTTAGTTG GGCATGGTGG
35151 CAGGTGCCTG TAATCCCAGC TACTTGGGAG GCTGAGGCAG GAGAATCGCA
35201 TGAACCTGGG AAGTGGAGGC TGCAGTGAGC CAAGATTGCA CCACTGCACT
35251 CTAGCCTGGG TGACAGAGCG AGACACCATC TTAACCAAAA AAAAAAATCT
35301 ACAATATACC AAAACCATTA CTTACCTGAG AAACATTTCT CAGGGTCATT
35351 GTAGTGAATG CCTATTTTAT GGCTTTTGAT GGCATCAGGG CACTCAGGTC
35401 ATTTACAAGA GTAGTGTGTG AGACCCTGTG TGTCACTGCC ACTCATCTTG
35451 GCCTTCGGCC ACTGCTGTAG CAACCAGTTT CCAAGTAGGG CTGGACCTTG
35501 CCTTCTGCTC CAGAGACCTC TCGCTTCCTG CCCTTGGGCT TCTGACGAGC
35551 TGACGGAAGT GCCTGGCAGG TGGGTCCCA CAACCCAGAG GAGGTGAGGG
35601 CCACCTCTCT GCTCCTCAGG GCCACCTTTC ATAAGGCTCC TTGAAGGTCC
35651 CTCAAGATCA AGCCAACCTA ACACATCCTT GATAGGCCTT CCTGCCCTCT
35701 GTTTCACCTT TCCACTCGTT TCCAAATAAA TGGCTGCATG CAAGCTTTTG
35751 CCTCAGGTTT TCCCTTTTAGG AGGAAGGCTA AGACAAGCAT TAAAGCAACA
35801 TGGGCAGGCA GAAGGATGAC TTCTAATAGA ATTATCTCAT CACTATATAT
35851 TTTACTTTAT GGATGCTTGT ATTGAAAAGT CTTGGCTGGG TGGAGTGGCT
35901 CACGCCTGTA ATCCCAGCCC TTTGGGAGGC CGAGGTGGGT GGATCACTTG
35951 AGGTCTGGAG TTTGAGACCA GCCTGACCAA CACTGGTAAA ACCTTGTCCTC
36001 TATTAAAAAT GCAAAAATTA GCCAGGGATG CACGCTTGCT GTGTGCCAGC
36051 ACAGGGCTAG CTGGGAGATA AAAAGGTGAG TAAGTAGGTC CGGTGTAGTC
36101 AGGGTGAAAA CTACAGATGG TCCATTTCCA CGTAAGTGGA AAGGTAAAGG
36151 TATGTACAAT AGGGTGGCTC CTGGCTGAAC CTGGAGCTGC AGACAGGTTT
36201 TCTAGAAGGC ATAATCCTGA AGTTGAGACT TGGGGGCTTA GGTAGGAGCC
36251 AGTTGAAGGG ACGTGGGAGG CGCATTCCAG AGAGAAGGAG TGGTATGAGA
36301 CTGGAACAGA GGTGTGCAGC AGCATCGCAT GGGCGAAACA ACAGTAGACA
36351 GTTGTCTTTT TGTTTTTGTG TGTTTTTTGA GACAGGTCTT TGTTCTGTCA
36401 TCCAGGCTGG AGTGCAAGTG CATGATCTCG GATCACTGCA ACCTCCACCT
36451 CCCAGGCTCA AGTGATCTTC CCACCCAGT CCCCAGTAG CTGGGGGACC
36501 ACAGGTGCAT GCCACGATGC CCGGCTAATT TTTGTACATT TTGTAGAAAC
36551 AGGGTTTTAC TGTGTTGTCC AGGCTGGTCT TAAACGCCTG AGCTTAAGCA
36601 GTCTACATGC CTCAGCCTCC TGAAGTGCTG GGATTCCAAA CATGAGCCAC
36651 TGTGCCTGGC CCGGCAACTG TTAGTAGACT ATAGAGAGGG AGGTGGGCAA
36701 GGGCTGGTGA CACTAGACAG GTGCAGTAGG TCTGGACCAT GGGTGGCCTT
36751 GCGCTACACA TTACAGAGCT CAGGCTTTTT TTCTCCAGGT GAGAGGGCTG
36801 GTGCCACTGA GGCATCAAGC AGAGGTTTGA GATCTCCTTG GTGACAGTGT
36851 AGAGCAGACA GGTAGATTTG GGAATTTAAG CTTAGACTCA CGTTGGAGAC
36901 TGAGATAGCT CATCTGAGAG GCACTCAGGG CCTAATCTCA GGCAGTAATT
36951 TTAGGGATGT AGGGGAAGAG ATGGATTCTG CACATACTTG GGAGGCTTGT
37001 GGAGGAGTGG GGAGGGAGGC ACAGGGAGGA CTCCAGGGTG GTTCATACGG
37051 CTCCCTGCTT CTGTTCTGTG CCCCCTTTGT CAAGCTGTGG TCTGTACTGC
37101 GTGTTCCATC TTGTTTCTAA GCTGCTTTTG CCCAGTCTTT CCAGCATTTT
37151 CCTTCGTCA TGTTAGTCTG TGCCTGTCTA CGTGAACAT GGTGACGTTT

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FIGURE 2L

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37201 ATTGGGCCTG GCACTGTGAG GTGCTGGGGA TGTGAAGATC ATTGTGGCTC
37251 AGCCGCTGCT CTCGAGGGCC TCTGGGTGCA GTATGCACAC CTGTGCCTCC
37301 TGTTTGCTCA GGAAGACAGG CTTTGAGATG AGCTGGGGCT GACATCCCCA
37351 CCTTATCATT GGGATGGCTT TGGGTAAGTT ATGTTTCATGT TCTCTGAGCC
37401 TCCCTTTCCT CATTGGTAAA ATGGGTATAA AATACCTGCC AGTGGAGGGT
37451 TGTGTAAAGT AGCCATGGAA AATGTAAAGC ACATAGCACT TACCATTTT
37501 TCCTGTGTCT TTAACAGATT TATCATAGAA TCCCGACTC AGACCATCT
37551 TCTAGCAAAA CAAGGCAGAT CATCTCCACC ATCCGGACGC AGAATCTTCC
37601 CAACTGTCAG CTGATTTCCC GAAGCCACTA CTCCCCATC TACCTGTCGT
37651 TTGTCATGCT TTTGGCTGCC CTGAGCTGGC AGTACCTGAC CACTCTCTCC
37701 CAGGTAACAG AAGACTATGT TCAGACTGGA GAACACTGAT CCCAAATTTG
37751 TCCATAGCTG AAGTCCACCA TAAAGTGGAT TTACTTTTTT TCTTTAAGGA
37801 TGGATTTTGT GTTCTCTTTA TTTTTTTCCT ACTACTTAA TCCCTAAAAG
37851 AACCTGTGTG GCTCGGACC TTTAGGAAAG TGAAATGCAG GTGAGAAGAA
37901 CCTAAACATG AAAGGAAAGG GTGCCTCATC CCAGCAACCT GTCCTTGTGG
37951 GTGATGATCA CTGTGCTGCT TGTGGCTCAT GGCAGAGCAT TCAGTGCCAC
38001 GGTTAGGTG AAGTCGCTGC ATATGTGACT GTCATGAGAT CCTACTTAGT
38051 ATGATCCTGG CTAGAATGAT AATTAAAAGT ATTTAATTG AAGCACCATT
38101 TGAATGTTCC TACTAGTAGA AAATGATGTG AATTTTCTT CTGTTCTGGCT
38151 CCTATTTTTT TCATCATTTT GTTTTCTTTA ATTGGGTGA ATGGAGTAGA
38201 TAGAAATATT TATGGTTTAG GTAACAGTTA GATGTTTCCT AAGAATGCAA
38251 ACTGCCTTTT CCACACAAAG GCTGGGAATA AAATCTGGG TATTCTCGTA
38301 TTCTCATTTA AAGGAGTTTA GCTTTCAGAG AGAAACAGCA GGATTGCTTT
38351 TGACCTTTTA GAAGATTGGT CTCCAGTAAA GGTGGACATT TTTGAGATTT
38401 TTATAATAAA GAATTTAATT GCTCTGCATT TGTCAAGTAC AGTTCGCTTG
38451 AAAGCCTGCC TGACTGTGGA AAAGATGGAG CTCAAGAATG GAGTTGATGG
38501 CCCAGCGTGG TGGCTCATGC CTGTAATCCC AGCACTTGG GAGGCTGAGG
38551 CGGTCGATC ACGACATTAG GGGATCGAGA CCATCCTGGC TAACACGGTG
38601 AAACCCCGT CTCTACTAAA AAAAAAAAAA ATTAGCCAGG CGTGGTGGCG
38651 GGTGCCTGTA GTTCCAGCTA CTCGGGAGGC TGAGGCAGGA GAATGGCTTA
38701 AACCCGGGAG GCGGAGCTTG CAGTGAGCTC AGATCGCGCC ACTGCACTAC
38751 CAGTCTGGGC AACAGAGCGA GACTCCATCT CAAAAAAGG AAAAAATTGT
38801 AAAAAAAAAA AAAAAAAAAA NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
38851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
38901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
38951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
39951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
40001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
40051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN (SEQ ID NO:3)
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FEATURES:  
Start: 2058

FIGURE 2M

Docket No. CL001201DIV  
Application Serial No. TBA  
Inventors: Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEIN...

Exon: 2058-2156  
Intron: 2157-7996  
Exon: 7997-8094  
Intron: 8095-8869  
Exon: 8870-9053  
Intron: 9054-25147  
Exon: 25148-25339  
Intron: 25340-29365  
Exon: 29366-29542  
Intron: 29543-30639  
Exon: 30640-30792  
Intron: 30793-37517  
Exon: 37518-37736  
Stop: 37737

**CHROMOSOME MAP POSITION:**  
Chromosome # 8

**ALLELIC VARIANTS (SNPs):**

DNA				Protein		
Position	Major	Minor	Domain	Position	Major	Minor
825	G	A	Beyond ORF (5')			
2632	C	T	Intron			
4430	C	T	Intron			
4791	C	T	Intron			
4886	G	C	Intron			
4887	A	T	Intron			
4889	T	A	Intron			
5110	G	T	Intron			
6911	G	A	Intron			
7212	A	G	Intron			
7355	C	T	Intron			
7398	T	C	Intron			
7653	T	C	Intron			
8310	A	G	Intron			
8145	C	T	Intron			
8031	G	A	Exon	45	R	K
8462	G	C	Intron			
8873	C	T	Exon	67	N	N
9190	C	T	Intron			
9311	T	-	Intron			
9847	T	C	Intron			
10460	C	T	Intron			
20204	G	A	Intron			
20362	C	A	Intron			
21166	G	A	Intron			
21477	G	A	Intron			
22230	C	T	Intron			
22941	A	G	Intron			
23963	C	T	Intron			
25686	A	C	Intron			
26018	A	G	Intron			
26078	G	A	Intron			
26625	C	G	Intron			
27151	C	T	Intron			
28032	G	A	Intron			
28772	G	A	Intron			
29572	C	T	Intron			
29761	C	T	Intron			
30732	G	C	Exon	281	L	L

FIGURE 2N

30841	G	T	Intron
31376	G	A	Intron
32032	A	G	Intron
32525	A	G	Intron
34179	G	T	Intron
34249	T	C	Intron
34451	T	C	Intron
34532	T	C	Intron
36541	T	C	Intron
36607	A	G	Intron
36681	A	G	Intron
37493	C	T	Intron
37966	C	A	Beyond ORF (3')
37973	T	C	Beyond ORF (3')
38113	C	A	Beyond ORF (3')
38298	G	C	Beyond ORF (3')

Context:

DNA

Position

825	GCAGTGAACGTACCTGACAGGTTTCCTGTTTGTGTTTTGAGATGAAGTCTCGCTCTTGTC CCCAGGCTGGAGTGCAATAGCGCGATCTCAGCTCACTGCAACCTCTGCCTCCTGTGTCA AGCGATTCTCCTGCCTCAGCCTCCCAGGTAGCTGGGATTATAGGCGCTGCCACCATGCC TGGCTAATTTTTGTATTTTAGTAGAGACGAGTTTCAGCATGTTGGCCAGGCTGGTCTT GAAGTCCAGACCTCAGGTGATCCGCCGCCCTTGGCCTCCCAAAGTGCTGGGATTACAGGC [G, A] TGAGCCACCGCGCTCGGCTAGACCTGACAGGTTTTAAAGGATTACTGGTTGCTGTGTTA AAACAGACTGCAGGATGGCTTAGGTAGCCAGTAGGTTTTTTTTTTTTTGGAGACGTAGT CTTGCTCTGTTGGCCTGGCTGGAGTGCAGCGGTGTCATCTTGGCTCACTGCAAACTCCGC TTCCCGGGTTCAAGTGATTCTCCTGCCTCAGCCTCCGGAGTAGTTGGGACTACAGGCCCC CACCACCACACTCGGCTTTTTGTATTTTAGTAGAGACGGGTTTACCATGTTGGCCAG
2632	GCCGCTCTGGCTGACCTGTCCCTGCCCGCAAGCCGCCCTGGGCATGAGCGACTTTTGC GTGGTTCCCGGTGGTTGCGCTCCCCGTTTCGTCCCCTCCGTGAGCATCGGCGCTTACCGG TATTTTAAACCGAGGGTTACACATCTGAGGCAATGTGGGTGGGTTACGCGGAGAGGACG AGTGAGTTTTTTGGTAAGCGGAATGAACTATGCAGATAACATCACATGAAGGCCGTTTCT GGAATGAAGTCTGACTCCTCCAGTTTACCACCTCTTCCGGAGCTCTCCCGCCTTGCTG [C, T] CTTCCATCGCTTCATCCTCGGTGCTTCTGAGTTTTTAAATCGCCTATCTACGCTTCCAA GTTCCAATGAGTTATCTAACGTCTATGGATTAGCTAGGTGGTTGGTGAAGGTCAGAACT TGGTTTTACTTAGATTTTTATCTGCCTCATGCCTGTACTATTTGTTAATGAATGCATAG GAGGTGTTTTTATTCACAAGAAAATTATTCGTACGCGATTATTGAATGAATAGACAAA TTCAGCCAAGTTCTTCTGGTCTGGACAGCCTGGCTGATTTCTGTAACTTTTTGGGCCA
4430	GGCCTTTTTTTTTTTTTTTTTTGTAGGGGGGGTCTCACTCCATCGTCCAGGCTAGAATGCT GTGGCCTGAACATGACTCACTCCAGTTTGAAGTTTCTTGGCTGAAGCCATCCTCCACCT CGGCTTCTGATCCCGAGTAGCTGGGACTCCAGGCACGTGTCACCAATGCATGGCTAATT TTTAAATTTTTTTGTAGACACAATGTCTCGCTGCATTGCCAGGCTGGTCTTGAATCCT GAGCTCAAGCGATTTTCCACCTCAGCCTTCAAAGTGCTGGGATTACAGGTGTGAGCCAC [C, T] GCACCCAACAGTTTCTCTGCAAACTAGGGAAAAAATTTACGCTTAGCAGATATTGAG GGCTGATTATTTCTATCACAGAAGCATTGGCTATAGAATTTAGGGTTTAGTAAACTTG ATTTACACTGAATTTTAGGTGCATATCAGTAAATCTACGGGCATATGCCGCCTGCAAGT TGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAAAGAGCAGGCTGTTAGTAATCAGGCA GATCTGGCTCCTGTCCAATCTAAATCCTGTTATTTAGACTAATATCTTAAGTCTGTTATT
4791	GGCTGATTATTTCTATCACAGAAGCATTGGCTATAGAATTTAGGGTTTAGTAAACTTG ATTTACACTGAATTTTAGGTGCATATCAGTAAATCTACGGGCATATGCCGCCTGCAAGT TGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAAAGAGCAGGCTGTTAGTAATCAGGCA GATCTGGCTCCTGTCCAATCTAAATCCTGTTATTTAGACTAATATCTTAAGTCTGTTATT AAGTCCGATTTCTGACGCTATTAAGTTAGGTGAACAACCTTGGTAACTTAACCTCTGAAC

FIGURE 20

[C, T]  
ACAGTTACTTCATCTGTAAAATAGGGATGTATGTATGGTAACGATTTTTTAACCACAAC  
TCCCAACTCTAAGATGGTCTGAAAAGAATTTTTTGAGTGTGGCTCAGAATCACTTGGC  
AGCAAAACCTGACTTGAAGTTGAGGCTTCATTATCCCACTTAGTATATTCAAATGTTTT  
GCTAAAGAAATAATTATGAGGTGCTACTTCACACTGACTAGGGTTGTATATGCATTTTAT  
TGCCATTTTTCTAAACACTAAAATGCTAAATTCTGCCCCAGGTCTTGCCACAGATGTT

4886 CTACGGGCATATGCCGCCTGCAAGTTGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAA  
AGAGCAGGCTGTAGTAATCAGGCAGATCTGGCTCCTGTCCAATCTAAATCCTGTATTT  
AGACTAATATCTTAAGTCTGTTATTAAGTCCGATTTCTGACGCTATTAAGTTAGGTGAAC  
AACCTTGGTAACTTAACCTCTGAACCACAGTTACTTCATCTGTAAAATAGGGATGTATGT  
ATGGTAACGATTTTTTAACCACAACCTTCCCAACTCTAAGATGGTCTGAAAAGAATTTTT  
[G, C]  
AGTGTGGCTCAGAATCACTTGGCAGCAAAACCTGACTTGAAGTTGAGGCTTCATTCAT  
CCCACTTAGTATATTCAAATGTTTTGCTAAAGAAATAATTATGAGGTGCTACTTCACACT  
GACTAGGGTTGTATATGCATTTTATTGCCTATTTCTAAAACACTAAAATGCTAAATTC  
TGCCCCAGGTCTTGCCACAGATGTTTCAGTGGACTATGGGCCTGTGAGACCTTAAAGGGT  
TGATTGAGTAAGGATCACAGGTGATGTCCGCATTGTGCTTGGCATGGAGTTAAGTGCTTG

4887 TACGGGCATATGCCGCCTGCAAGTTGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAAA  
GAGCAGGCTGTAGTAATCAGGCAGATCTGGCTCCTGTCCAATCTAAATCCTGTATTTA  
GACTAATATCTTAAGTCTGTTATTAAGTCCGATTTCTGACGCTATTAAGTTAGGTGAACA  
ACCTTGGTAACTTAACCTCTGAACCACAGTTACTTCATCTGTAAAATAGGGATGTATGTA  
TGGTAACGATTTTTTAACCACAACCTTCCCAACTCTAAGATGGTCTGAAAAGAATTTTTTG  
[A, T]  
GTGTTTGGCTCAGAATCACTTGGCAGCAAAACCTGACTTGAAGTTGAGGCTTCATTCATC  
CCACTTAGTATATTCAAATGTTTTGCTAAAGAAATAATTATGAGGTGCTACTTCACACTG  
ACTAGGGTTGTATATGCATTTTATTGCCTATTTCTAAAACACTAAAATGCTAAATTC  
GCCCCAGGTCTTGCCACAGATGTTTCAGTGGACTATGGGCCTGTGAGACCTTAAAGGGT  
GATTGAGTAAGGATCACAGGTGATGTCCGCATTGTGCTTGGCATGGAGTTAAGTGCTTGA

4889 CGGGCATATGCCGCCTGCAAGTTGTGTGGCATCACCCAAAAGCCGAGAGTAATGGAAAGA  
GCAGGCTGTAGTAATCAGGCAGATCTGGCTCCTGTCCAATCTAAATCCTGTATTTAGA  
CTAATATCTTAAGTCTGTTATTAAGTCCGATTTCTGACGCTATTAAGTTAGGTGAACAAC  
CTTGGTAACTTAACCTCTGAACCACAGTTACTTCATCTGTAAAATAGGGATGTATGTATG  
GTAACGATTTTTTAACCACAACCTTCCCAACTCTAAGATGGTCTGAAAAGAATTTTTTGAG  
[T, A]  
GTTTGGCTCAGAATCACTTGGCAGCAAAACCTGACTTGAAGTTGAGGCTTCATTCATCCC  
ACTTAGTATATTCAAATGTTTTGCTAAAGAAATAATTATGAGGTGCTACTTCACACTGAC  
TAGGGTTGTATATGCATTTTATTGCCTATTTCTAAAACACTAAAATGCTAAATTCGTC  
CCCAGGTCTTGCCACAGATGTTTCAGTGGACTATGGGCCTGTGAGACCTTAAAGGGTTGA  
TTGAGTAAGGATCACAGGTGATGTCCGCATTGTGCTTGGCATGGAGTTAAGTGCTTGATA

5110 AAATAGGGATGTATGTATGGTAACGATTTTTTAACCACAACCTTCCCAACTCTAAGATGGT  
CTGAAAAGAATTTTTTGAGTGTGGCTCAGAATCACTTGGCAGCAAAACCTGACTTGAA  
GTTGAGGCTTCATTCATCCCACTTAGTATATTCAAATGTTTTGCTAAAGAAATAATTATG  
AGGTGCTACTTCACACTGACTAGGGTTGTATATGCATTTTATTGCCTATTTCTAAAACA  
CTAAAATGCTAAATTCGCCCCAGGTCTTGCCACAGATGTTTCAGTGGACTATGGGCCT  
[G, T]  
TGAGACCTTAAAGGGTTGATTGAGTAAGGATCACAGGTGATGTCCGCATTGTGCTTGGCA  
TGGAGTTAAGTGCTTGATAAATGGTGGTTATCAATCTGATTATGTAAATTTATGTAAATT  
CAGTTCTCAAGTTTGTGGTTTTTTTCCCTCCTGGAGAAATCTATTCTATTTTAAAGTGA  
GGAAGGCTCCGTGGAGGCTGGTAGCTGTGAGTCTTCACTTGTGGAACCTTCAGCCTGA  
GGCTGGAGCCCCCTTCTGGGAGTCTGGTCTTGTGCTTCTTGACACCCCCACACCTT

6911 CCACCTTGGCCTTCCGAAGTGCAGGGATTATAGGCGTGCGCCACTGCACCCGGCCCTGTT  
GGATAAATGATTCCAGTCTCTCCCAAAAAGAACTGTTGTAAGACTGTGGGGTGAGGGGAG  
GGAAGGGACAAATAGGAACCCGCGTATTTTCCACTCCCTGTGGGCCTAAAACGTCTCTA  
AAAAATAGTCCATGAAAAAATACATAGTACAAACAGCAACTCTTCTGATATGCTTGCAT  
TAAAAATCAGGCTTTTTCTCCCTTTTGGAAAAACACAGTCTTGTGTGCTTTAGGGAAGA  
[G, A]  
TAAAGGTCAGTGCCTGCATTGCATTAATTTGAAGGGAAAGATGAGAAGACATCTTGAA

FIGURE 2P

AGGAATGGCTGGCTTTCTAGAGAATAGTAGAGGCTTAATAGGTGTCATAGAAAAACCAGG  
GTTGGACAGTGGTAGTAAAACGGCAAAACAGATTTTATTAGAAAACTACTGCAGTAAG  
AGGAGAGAGACCTCGGTACAGAACTGCTCCACTGCGAATACAAAGAAAAGTAGGAATTGA  
TGGCGGGGAGCCGGATGTCTAGTGGATGGAATAATTATTACGAGGAAACACAGGGGTGTGC

7212 TAAAGGTCAGTGCCTGCATTGCATTAAATTTTGAAGGAAAGATGAGAAGACATCTTGAA  
AGGAATGGCTGGCTTTCTAGAGAATAGTAGAGGCTTAATAGGTGTCATAGAAAAACCAGG  
GTTGGACAGTGGTAGTAAAACGGCAAAACAGATTTTATTAGAAAACTACTGCAGTAAG  
AGGAGAGAGACCTCGGTACAGAACTGCTCCACTGCGAATACAAAGAAAAGTAGGAATTGA  
TGGCGGGGAGCCGGATGTCTAGTGGATGGAATAATTATTACGAGGAAACACAGGGGTGTGC  
[A, G]  
TTCTTGCTGAAGGCAGGCCAGAGTTATCAGACATCACCTGAGGGATGGAGGGGGATGTGG  
AACCTAATCGGCTGTCTAGGGTGATCAGATACTGAAGTTGGGGGATTCTGGTCAAATCAA  
TTTAGCAGGATTCTTGGTAAAACCTGGGCGATGCAAAGACAGATGCGTTGAGTACAAAGTC  
CAGGCTTTATTGGGAAGAGGATTTTCAGCGGAGCCCGAGTAGAGTTTGGTCTAGGGAGACT  
CTGTCACTGGGAGGACGAGCGAGCCGCTCGGAAGTGCCTGGGTTCTTTAGCGGCCAGT

7355 CAAAACAGATTTTATTAGAAAACTACTGCAGTAAGAGGAGAGAGACCTCGGTACAGAA  
CTGCTCCACTGCGAATACAAAGAAAAGTAGGAATTGATGGCGGGGAGCCGGATGTCTAGT  
GGATGGAATAATTATTACGAGGAAACACAGGGGTGTGCATTCTTGCTGAAGGCAGGCCAGA  
GTTATCAGACATCACCTGAGGGATGGAGGGGGATGTGGAACCTAATCGGCTGTCTAGGGT  
GATCAGATACTGAAGTTGGGGGATTCTGGTCAAATCAATTTAGCAGGATTCTTGGTAAAA  
[C, T]  
TGGGCGATGCAAAGACAGATGCGTTGAGTACAAAGTCCAGGCTTTATTGGGAAGAGGATT  
TCAGCGGAGCCCGAGTAGAGTTTGGTCTAGGGAGACTCTGTCACTGGGAGGACGAGCGAG  
CCGCTCGGAAGTGCCTGGGTTCTCTTAGCGGCCAGTGGGTTCTGGTGAGAAGGGCAACA  
GCGGGAGGAGCGCCGCTGCGGAGCGGAGGCCGGGGGCGGGGCTGCGGGGCTGCGGGGC  
GGGCCCCGTTGTGGGTGCGCCAGCGCTATTGAGTAGAGGGCGAGCCCGTCCCGCCTCT

7398 GAGACCTCGGTACAGAACTGCTCCACTGCGAATACAAAGAAAAGTAGGAATTGATGGCGG  
GGGAGCCCGATGTCTAGTGGATGGAATAATTATTACGAGGAAACACAGGGGTGTGCATTCTT  
GCTGAAGGCAGGCCAGAGTTATCAGACATCACCTGAGGGATGGAGGGGGATGTGGAACCT  
AATCGGCTGTCTAGGGTATCAGATACTGAAGTTGGGGGATTCTGGTCAAATCAATTTAG  
CAGGATTCTTGGTAAAACCTGGGCGATGCAAAGACAGATGCGTTGAGTACAAAGTCCAGGC  
[T, C]  
TTATTGGGAAGAGGATTTTCAGCGGAGCCCGAGTAGAGTTTGGTCTAGGGAGACTCTGTCA  
CTGGGAGGACGAGCGAGCCGCTCGGAAGTGCCTGGGTTCTCTTAGCGCCAGTGGGTTC  
TGGTGAGAAGGGCAACAGCGGGAGGAGCGCCGCTGCGGAGCGGGAGGCCGGGGGCGGGG  
CTGCGGGGCTGCGGGGCGGGCCGCTTGTGGGTGCGCCAGCGCTATTGAGTAGAGGGC  
GAGCCCGTCCCGCCTCTCGTGGGCGCTTCCAGATCTGCTTGAGTCTATGGAGGAAAA

7653 AACTGGGCGATGCAAAGACAGATGCGTTGAGTACAAAGTCCAGGCTTTATTGGGAAGAGG  
ATTTTCAGCGGAGCCCGAGTAGAGTTTGGTCTAGGGAGACTCTGTCACTGGGAGGACGAGC  
GAGCCGCTCGGAAGTGCCTGGGTTCTCTTAGCGGCCAGTGGGTTCTGGTGAGAAGGGCA  
ACAGCGGGAGGAGCGCCGCTGCGGAGCGGGAGGCCGGGGGCGGGGCTGCGGGGCTGCGG  
GGCGGGCCGTTGTGGGTGCGCCAGCGCTATTGAGTAGAGGGCGAGCCCGTCCCGCC  
[T, C]  
CTCGTGGGCGCTTCCAGATCTGCTTGAGTCTATGGAGGAAAACTCCGCGGGGTCCGC  
GATTCCCATGGCCGAGCCGCTGCGGCACCAAGGCCATGGCCCTCTTCAAGCGCACCTT  
GGTGTGAGTCCCGCCGCGCGCCAGGGGCCCGGGCGCAGGCACCGCCCGCGGGGCTG  
CTGCTTGCTCTGCGCCTGGCCCTGCAAGGACTGGCTCGGGGAGAGGGCGGCAGGCT  
GTGGAGCCGCTGCCCCAGTCCAGTCCCACTCCCACTCCCACTCCCACTCCCACTCCCTG

8310 CAGCCTGAAAACTTGCTACAAAGTATCTCAATCAGACCAGTCGAGTTTCGAGCTGTTAT  
CCAGGCGCTGGATGGGGAAATGCGGTGAGTGATGGAGGCAGCGCCTCTGGCTTGGAGGAA  
AGCTTGCTCCGGGACTTTTGTAGTGTGTTGGAAGCTACCTTTTGATATAGCGCTCAGCGTTG  
CAGCCTCGTTGCTGTGGCTTATCCAGAACATAGCCCGGCCCTACGTGTTACTTTAGAAA  
GCCCTTCCAGGCTCTTTGCCATCTAGTAGAGTCCCTGCGGGCCAGCCTTTCAGAGAAG  
[A, G]  
GGGGGAGGGGGTGATGTTTATTAACCTTTTGTAGTCTTGGCAGCTGAACCTGCCTGTGA  
GCAGGTGCTGATTTCTCGGCTTCCCTTATCCAACCTTGCATTTCTATTTCTAGCATATT  
GGGTTGATTCTTTGAAGCTGCCTCTGTGCACATTACACCCATGAACCTAGACCAGTTGC

FIGURE 2Q



CTTTATGTATGATCGTATTTATACTGAGAAAGTTACTGTGTTTTTTGACTTTCTTTTCTAT  
TTGCTACATATTAGTTCGGTCTAAACGTTTGGTCTTCTGGTCTCCATAGTTCTACATTG

8145 CAGCCTGAAAACTTGCTACAAGTATCTCAATCAGACCAGTCGCAGTTTCGCAGCTGTTAT  
CCAGGCGCTGGATGGGAAATGCGGTGAGTGATGGAGGCAGCGCCTCTGGCTTGAGAGAA  
AGCTTGTCCGGGAC  
[C, T]  
TTTGAGTGTGTTGGAAGCTACCTTTTGATATAGCGCTCAGCGTTGCAGCCTCGTTGCTGT  
GGCTTATCCAGAACATAGCCCGGCCCTACGTGTTTACTTTAGAAAGCCCTTCAGGCTCT  
TTGCCATCTAGTAG

8031 CAGCCTGAAAACTTGCTACA  
[G, A]  
GTATCTCAATCAGACCAGTC

8462 GCTACCTTTTGATATAGCGCTCAGCGTTGCAGCCTCGTTGCTGTGGCTTATCCAGAACAT  
AGCCCGGCCCTACGTGTTTACTTTAGAAAGCCCTTCAGGCTCTTTGCCATCTAGTAGAG  
TCCCTGCGGGCCAGCCTTTCAGAGAAGGGGGGGAGGGGGTGATGTTTATTAACTTT  
TTAGTCTTGGCAGCTGAACCTGCCTGTGAGCAGGTCGTGATTTCTCGGCTTCCCTTATC  
CAACTTTGCATTTCTATTTCTAGCATATTGGGTTGATTCTTTTGAAGCTGCCTCTGTGCA  
[G, C]  
ATTACACCCATGAACCTTAGACCAGTTGCCTTTATGTATGATCGTATTTATACTGAGAAGT  
TACTGTGTTTTTTGACTTTCTTTTCTATTTGCTACATATTAGTTCGGTCTAAACGTTTGG  
TCTTCTGGTCTCCATAGTTCTACATTGGTTAAATGCAACTCACTTCTGGGAGTAGTGGTG  
ACATTCAACTAGTAGGCTTTTAAATAAACTACAGAAGTTCATTACTCTCATGTAAGGAAG  
GAAACTAATGTAACCTTCGTAAAGTATGAAAAGCGTTGGATATCCTTATAGTTCTTTAG

8873 AAACGTTTGGTCTTCTGGTCTCCATAGTTCTACATTGGTTAAATGCAACTCACTTCTGGG  
AGTAGTGGTGACATTCAACTAGTAGGCTTTTAAATAAACTACAGAAGTTCATTACTCTCA  
TGTAAGGAAGGAAAACTAATGTAACCTTCGTAAAGTATGAAAAGCGTTGGATATCCTTAT  
AGTTCTTTAGAGTTAAGGGTGAGATGGGTTTAGAAAGTGGCCAGGCACAAGTTATTTTAA  
AATAAAAAATCTTTGGCTGTTTGTTCCAATATATTAATAGTTTTCCCTTTTTTACAGCAA  
[C, T]  
GCAGTGTGCATATTTTTATCTGGTTCTCCGAGCTCTGGACACACTGGAAGATGACATGACC  
ATCAGTGTGGAAGAAGGTCCCGCTGTACACAACCTTCACTCTTTCCTTTACCAACCA  
GACTGGCGGTTTCATGGAGAGCAAGGAGAAGGATCGCCAGGTGCTGGAGGACTTCCCAACG  
GTGAGTGGGTTACGCATCTTGTCTACGACTGTTGTGTTTCATAATTGCTAACGTGGTTG  
TCCGGTAGCCTCCATACATGTGGAGAAAGGTTAAATAAGCATTCTGAGGGCAGCATAATGTGAGGGTAAAAACTC

9190 ATCTGGTTCTCCGAGCTCTGGACACACTGGAAGATGACATGACCATCAGTGTGGAAGA  
AGGTCCCGCTGTACACAACCTTCACTCTTTCCTTTACCAACCAGACTGGCGGTTTCATGG  
AGAGCAAGGAGAAGGATCGCCAGGTGCTGGAGGACTTCCCAACGGTGAGTGGGGTTACGC  
ATCTTGTCTACGGAAGTGTGTGTTTCATAATTGCTAACGTGGTTGTCCGGTAGCCTCCATA  
CATGTGGAGAAAGGTTAAATAAGCATTCTGAGGGCAGCATAATGTGAGGGTAAAAACTC  
[C, T]  
GGTAGCCAAGACTCTGAAGCCAGGCTGCCTGGGTTGGAATCTCAAATCTCCCACTTACTA  
AACTGTTGGTTACTTACAAAGACTCTCTGTGCCTCAGTTTCTTCATCTGTAAAATAGGGG  
TAATAATAACACCTACCTCATGGTATTCTGAGGATTCAAAGAATTAACGTAGGTAATGCT  
CTTAGAATGTAGCTACTGCTGTTATTATCAGTATTGGAAGTCCAGTGTTCCTCCTGTG  
GGAAGACGCAGTCAAATTTTAGTGTTGTGAAAGATTCTCAGGCTAGCTCACAAAAGCCTG

9311 GAGCAAGGAGAAGGATCGCCAGGTGCTGGAGGACTTCCCAACGGTGAGTGGGGTTACGCA  
TCTTGTCTACGGAAGTGTGTGTTTCATAATTGCTAACGTGGTTGTCCGGTAGCCTCCATAC  
ATGTGGAGAAAGGTTAAATAAGCATTCTGAGGGCAGCATAATGTGAGGGTAAAAACTCC  
GGTAGCCAAGACTCTGAAGCCAGGCTGCCTGGGTTGGAATCTCAAATCTCCCACTTACTA  
AACTGTTGGTTACTTACAAAGACTCTCTGTGCCTCAGTTTCTTCATCTGTAAAATAGGGG  
[T, -]  
AATAATAACACCTACCTCATGGTATTCTGAGGATTCAAAGAATTAACGTAGGTAATGCTC  
TTAGAATGTTAGCTACTGCTGTTATTATCAGTATTGGAAGTCCAGTGTTCCTCCTGTGG  
GAAGACGCAGTCAAATTTTAGTGTTGTGAAAGATTCTCAGGCTAGCTCACAAAAGCCTGC  
CGACTGTATGATGCAGCCTACCTGTAACACTGCTGGCCTCTTGACTACCCGGAGCCTGGT  
AGCATGGGACTGCTGCTCACGATGGGCAGCAGCCTGGCATGGGGCGGTGTCTGTTGGCA

FIGURE 2R

9847 CTGGTAGCATGGGACTGCTGCTCACGATGGGCAGCAGCCTGGCATGGGGGCGGTGTCTGT  
TGGCAGCTAGGGCGAGCCTCTGCCACTTCACCTGTGATCCTGGGCAAGTTCCTTATCTGC  
TTTGTGTCTCCGTCTCCTCGTTTTGTAAAGTTAGAGCTGAGAGGATTAATTTTCGCACATAT  
AAAGTACTTAGTGCCTGGTACAGGTAAGTATTCTGTAAGTATTAGCTATTTGGTCTATT  
TTGTTGGAGTAAAGTGGGTATAGTTAAATCCTAAGATTTTTAAAGTCCCTCAAGTTCA  
[T, C]  
GTGGACATCTGCCTAGGTCTACTATCCTAGAATTCGCATGTCTTATCACACAAATAACT  
GATTCTTCCATATCTTATAAATAAAGGTTTGATTTAGCAAAGTCACATGTTGTGTAATAG  
CTCGAAGAGCCCTTTTGTCCACAGTTGCCAGAGCTTTTGGAGAACAGTCCTTATGTTA  
TTGAAACAAACCTAATCTGTAGCTGAGTTGGGAGGGAGCTAAGTGGACAGAGAGTCCTCC  
ACCCAAACAAAAGAATCTTTGATTCTTGGGCATAATGGGAGCAATATTTAAAAA

10460 AGGAATGTTTGGGGAAGACTCTTGCGGTGCAAAGGCTGTTTCAGATTGCTGAGATCAGAC  
CTTAAGTACCAAAGCCCAAATATAGTACAACATAATACAAATGAGAAGAAAATAGCTGAA  
GAATAATTCGAGTTTATACAGTACAATTCAAGAGAAGAAAGAAAATTTATGACGACTAGC  
TGGGTGAGAATTAGAACTGTAACCCCTGGGAAGGTCCTGGTGATTTGACTCTCACAGGACA  
CCTGATGACCAGAGGATGGGTTTCTTTGATGGGAAATCTGTGGCGATTTCATTGATGGGC  
[C, T]  
TCTGAATCTGCTGAAGCAGAGGAAGTAGTAATACCCATTTATAATGGAAGTGCATTCT  
CACTTAAAAACAATAATATTATTCTAGCTGGACCTAGCCTCTAGAAAACAGCCAAATTAC  
ATTTGACTTGAGTGGATTCAATAAATAAAAAATTTCTGGGCGATGGGATAAATGTGTT  
AGGTATTGCTAAGTCAAGGCAGCCCTATCCCTCAGCAGAAGTGAGGGAATATGAAAGTG  
TGTGAATGCTAACATAAATTTTGGGGAATATCGCCGTCAGATTTCCAGATGATATTCACAC

20204 TCTGCCAGTTGCGAAGACTGGGAAAAGCACAGTATTGGGCAGAGTATACTGTTCTCCTCA  
GGTACAGTCACTCACGCCCTTCTCTGGCTAGGAAAGGGAATCCCTGACCCCTTGCACT  
TCCTGGATGAGGTGACGTCCTGCCCTGCTTTGGCTCACCCCTCCATGGGCTGCACCCACTG  
TCCAACAGTGCCAATGAGATGAACCAGGTACCTCAGTTGGAATGCAGAAATCACCCAT  
CTTCTGCATCGATCTTGCTGGGAGCTGTAGACCAGAGCTGTTCTCTACTGGGGCATCTTGG  
[G, A]  
AGCAACTCTGGGTCTGAGTTTCTGTTTGTGTCCTGATGTATATCCCCAGTGCCTAGAAT  
GATACTTGTATACATAGGAAGTGCTTGATCCATGTTTGCACAAATGAATCTTTCTCATAAT  
GAGGTTTCTCTAAACAAGCTGTTCTCCCAAAAACCTTACACCCAGCTTTATGTTGAAGCAT  
CTCATTATACATTGGAAGATGAAATGTGTAGTGAGACTTTGAATCTTCTTTTGAATCTA  
GAAACATTAGCATTTTTAGACCATTCTATTTTAATATTTATGAAATTTATGAAATAATAA

20362 CCTCCATGGGCTGCACCCACTGTCCAACAGTGCCAATGAGATGAACCAGGTACCTCAGT  
TGGAAATGCAGAAATCACCCATCTTCTGCATCGATCTTGCTGGGAGCTGTAGACCAGAGC  
TGTTCTTACTGGGGCATCTTGAAGCAACTCTGGGTCTGAGTTTCTGTTTGTGTCCTGA  
TGTATATCCCCAGTGCCTAGAATGATACTTGTTACATAGGAAGTGCTTGATCCATGTTTG  
CACAAATGAATCTTCTCATAATGAGGTTTCTCTAAACAAGCTGTTCTCCCAAAAACCTTA  
[C, A]  
ACCCAGCTTTATGTTGAAGCATCTCATTATACATTGGAAGATGAAATGTGTAGTGAGAC  
TTTGAATCTTCTTTGAATCTAGAAACATTAGCATTTTATAGCATTCTATTTTAATATT  
TATGAAATTTATGAAATAATAAGAAACATGAGGCCGGGCTCAGTGGCTTATGCCTGTAAT  
CCCAGCAGTTTGGGAGGCCAGGGCTAGTGGATCATGAGGTGAGGAATTTGAGACCAGCTT  
GGCCAACATGGTGAAACCCCACTTCTACTAAAAATATAAAAATTAGCTGGGCGTGGTGGT

21166 TAATTCGCCCATGTTTGCCTTGTGATCTTTGGTGCCATGTCTGTACATATTTTCATGATT  
TCTGTGTTTTTACGGTTTCCATTTAGATCTCCCTGAGTTTAGAAATCTGGCTGAGAAA  
TACCAAACAGTGATTGCCGACATTTGCCGAGAAATGGGCATTGGGATGGCAGAGTTTTTG  
GATAAGCATGTGACCTCTGAACAGGAGTGGGACAAGGTTAGTCTCATAAAACAGTGTCTG  
TGTGTGATGTATTAGACAGAGCTGGCAGTCTCATAGTGAAGCTCAGAACAAGAAAAGTT  
[G, A]  
TCCAGTATTTTTCAGCCCTCTGGTTTTTACAATTCATCTGTTTAGGTTGAATGTCTCATCA  
TAAACAGTTTATTCAGAGTTAATCCAAACAGCAGCTATGTAGGATATCAGCCAGGCT  
AGGAGTAGGGTACTGGAGAGAAGTGCTTATCTAGACAAAGGGATGTAATTGACCATGAAG  
ATTAAAACATACACATCAAAACATAAGGTAGGGTTAGGAGTCTTGCCATTTTTTTCATAGGA  
ATGGTGTTTGTGAGACTTACTCATCACTTCTGTGGAAGTAAAGACATTTTATTTATTTAT

21477 TCAGCCCCCTCGGTTTTACAATTCATCTGTTTAGGTTGAATGTCTCATCATAACAGTTT

FIGURE 2S

ATTCCAGAGTTAATTCCAAACCAGCAGCTATGTAGGATATCAGCCAGGCTAGGAGTAGGG  
TACTGGAGAGAAGTGCTTATCTAGACAAAGGGATGTAATTGACCATGAAGATTAACCTA  
CACATCAAAACATAAGGTAGGGTTAGGAGTCTTGCCATATTTTTCATAGGAATGGTGTG  
TGAGACTTACTCATCTTCTGTGGAAGTAAAGACATTTTATTTATTTATTTTAAAGCCA  
[G, A]  
TCAGATTTAGCAGGCAGAGACATTTTCAGACATCTAAAGTGTTGATGTATTTTCATACCTTT  
AACTGTGCTTAAATTAGGATCTCCGAAAAGATGCTGCTACATGGTCACTACGTTAGTGTA  
GGTCCAAGGTCTTGGGCCTCTTAATTTTCAAACCTCAAACTTGACAGCAGTTATCTTT  
GGAACGTGCTGATTTGTGCTTCTTAAGTTAACAGCATACAATGACTGCTAGAAATCAATTT  
CTGCATTTAAGGTGAAGTTAGCCGGGTACTATGGTTTACCTGTAATCTCAGCACTTTGGG

22230 GGATTGCTTGAGCCCAAGAGTTGAAGGTTGCAGTGAGCCATGATTGTGCCACTGCACTCC  
AACGTGGGTGACAGAGCAAGACACCTACTGAAAGAAAATAAAGTTGAAGTTAAACCTTCT  
GGCCAAGAACCAGCACTGGTTATGATAGTAACCTATTTTCTGTTGTGCAGATTTATTCAG  
GAACTTAATTTTAGGTTGTTGAATAGAAGTTTGTATCAGATAAAATTGAATTAACAAAA  
ATTTTTTTTGAGACAGGGTCTTGCTGTTATCCAGGCTGGTGTGTAGTGGTGTGATCACGG  
[C, T]  
TCCCCGCAGCCTCAACCTCCTGGGCTCAGGTGATCCTCCACCTCAGCCTACCGAGTAGC  
TGTAACCTACAGTGCTGACACCATACCAGGCTCATTTTGTACATTTTGTAGAGAGAG  
GGTTTTGCCATGTTGCCAGGCTAGTCTCAAACCTCCTGGCATCAAACAGTCTCCCACTC  
TGGCCTCTCAAATGTTGGGATTACAGGCATGACCAGCCAATTATTTCAAGGAGTTATTTT  
TTTTCTCTACTTTGGGGGAAGATGAATTATATAAGTCTCCATTTTAGGAGTATTTCTAC

22941 AATTTCTGTCTACCTAATTTTCAGCAAGATTTCACTCTTTTCATGTTACTTTTGTCCCAGA  
ACAAATTTCAAGTGCTTCTCTTCACCTGTGCATTCTTCCCCCTGATTAGTCTCTGGCTT  
TGTAATTACTTTTCAGTCAGAGACGACTTTTTTTTTTTTGAGACAGGGTCTCACTCTGTCA  
CAGACTGGAATGCAGTGGCACAGACAAGGCAGCCTTGACCTTCTGGGCTCAAGCAATCTT  
CCTTGCCCTCAGCCTCCTGAGTAACCTGGGACCACAGGCACGTTGCCACCATGCCTGGCTA  
[A, G]  
TTTATTTTAATTTTTATTATTTTTTGAGACAGGGTATTGCTCTGTCAACCAGGCTGGAGTG  
TAGTGGCATGATCAAGGCTCACTGCAGCCTTCACCTCCTGTGCTCAAGCAGTCTCTCTAC  
CTCAGCCTCCCCATTAGCTGGGACTATAGGTCCACACCACTACACCAGGCTAATTTTGT  
AATTTTTTGGTAGAGACAGGGTTTCATCGTGTGCTAGGCTGGTCTTGAGCTCTGGGC  
TCAAGCGATTACCTGCCTTAGCCTCCAGGTGTGAGCCACTACACTCAGCCTTTTAAAA

23963 ATACTACCTAGTTTTGAACCTTTAGCCCCCTGCCACAGACACGGCAGCCCCCTTGAACCTTC  
CTGGGTTCAGCGAGCCTCCTACTTCAGCCCCCTGAGTAACCTGGGACCACTGGCCTGTGT  
CACTGTGCCTGGCTAATTTTTTTTTTCTCCTCACATGGGCAATGTTGGGCAAGTTAAATC  
GACTTCTTTGTGCTCAGTTTCTCATCTGAAATGGAGATCATACTGCTATGTACCTGAT  
ACAATGTTTGTGAGGATTGAATGTGCAGAGTTCCTTTTTTCTGTTGTTGTTTGTGAGA  
[C, T]  
GGAGTCTCACTCTG

25686 CTGAAAAATCCTTTAACTCTTGTGGTTGCGGGTGACAGAAAAACAAGCCAGGCCTCCCC  
AGGCAGCATAAAGGGATGTGGAATAAGGATAGATTGACATGAGTTTGCTTCAGGTAGAC  
TGGCTGACTCCAGGATTACACACCGTAATCAGTATATTCAAGCCTTGCTGTCTTGAT  
TTCTTTTTCAGACGGTCTTTCTCCAAGTGGTGGATATGGTAACAACCCAGTGCCTAGCTT  
AACAAAAAGTTCTTAGGAATGGCTTTGTTGCGCCTGGCGCAGTGGCTCATGCCTGTAATC  
[A, C]  
CAACAGTTTGAGAGGCCAAGGTGGGCGGATCACCTGAGGCCAGGAGTTGAGACCAGCCT  
GGCCAACATAGTGAAACCCCGTGTTACTAAAAATACAAAAATTAGCCGGGCGTGGTGG  
CAAGGGCTTGTAATCCAGCTACCTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGG  
AAGCAGAGATTGCGGTGAGCTCAGATTGTGCCACTGCACTCCAGCCTGGGCGACAGAGTG  
AGACTCCCTCTCAAAGAAGAGGAAGGGCTTGGTTCTTCTGCTCAGCCCTGAATCAGTTA

26018 ACCTGAGGCCAGGAGTTTCGAGACCAGCCTGGCCAACATAGTGAAACCCCGTGTTTACTAA  
AAAATACAAAAATTAGCCGGGCGTGGTGGCAAGGGCTTGTAATCCAGCTACCTGGGAGG  
CTGAGCAGGAGAATCGCTTGAACCCAGGAAGCAGAGATTGCGGTGAGCTCAGATTGTGC  
CACTGCACTCCAGCCTGGGCGACAGAGTGAGACTCCCTCTCAAAGAAGAGGAAGGGCTT  
GGTTCTTCTGCTCAGCCCTGAATCAGTTACTGTTGCTACACAGCTGAGTTCTCTGGCCTC  
[A, G]  
CCTGGATTACGTCTACACAGTACACACAGAATGGATTTCACCCCAAAGAAAGAAATCTGCG

FIGURE 2T

GCAGGAAGGGGAAAGGGATGGCAGGTAGACAAAACTCCAGGTGTCTGTAATAAGGGACA  
GGGTCGATCTTTAATTAAAACATGGACAGGGAACAGAAAGCTTTTGATACTGATTTGT  
CAGAAGGAAAGTAGAAAATTTTATGACTGTTCCCTGAATTTATTCCAGCATTTACCTTT  
GCTTTCCATAAAAGTGTTCCTGCAGCCAAGTACTTTAAAGTTTAAAAAGACGGGTGAG

26078 AAAATACAAAAATTAGCCGGGCGTGGTGGCAAGGGCTTGTAAATCCCAGCTACCTGGGAGG  
CTGAGGCAGGAGAATCGCTTGAACCCAGGAAGCAGAGATTGCGGTGAGCTCAGATTGTGC  
CACTGCACTCCAGCCTGGGCGACAGAGTGAGACTCCCTCTCAAAGAAGAGGAAGGGCTT  
GGTTCCTCTGCTCAGCCCTGAATCAGTTACTGTTGCTACACAGCTGAGTTCTCTGGCCTC  
ACCTGGATTACGTCTACACAGTACACACAGAATGGATTTCCCCCAAAGAAAGAATTCTGC  
[G, A]  
GCAGGAAGGGGAAAGGGATGGCAGGTAGACAAAACTCCAGGTGTCTGTAATAAGGGACA  
GGGTCGATCTTTAATTAAAACATGGACAGGGAACAGAAAGCTTTTGATACTGATTTGT  
CAGAAGGAAAGTAGAAAATTTTATGACTGTTCCCTGAATTTATTCCAGCATTTACCTTT  
GCTTTCCATAAAAGTGTTCCTGCAGCCAAGTACTTTAAAGTTTAAAAAGACGGGTGAG  
GCTAAGTGTGGTGTCTCATACTTATAATCCCAGTGTCTGAGGCCAGGAGTTCAAGACCAGC

26625 TGTGGTGTCTCATACTTATAATCCCAGTGTCTGAGGCCAGGAGTTCAAGACCAGCCTGAGC  
AACACAGCAAGATACCATCTCTATAAAAAATTGTTAGAAAATGATTCTGCTGAAAGAGCA  
AAAATAAAAATTAAAGAAAGTAGAAAAATAAACTAAATTTAAAGATTAACCTGGGCAT  
GTTGGCATGCACCTGTATTCTTAGGTATTCTGGGAGGCTAAGGCACAAGGATCCCTTGAGC  
GCAGGAGCTCAAGGTTGGATTGAGTTGTAATCACACCACTGCACTCCAGCCTCGGTGGCA  
[C, G]  
AATGAACTGTCTCAAGAAAAAAAAAAGTGACAGAGGGAAACAATATTTGCAATTCATA  
GAGCAGATACAGGGTTCATATTCTAATATTAAAAAACTTCTAAAAGTTAAGAAAAAG  
GCCAACTGCCCCACAGAAAAATGGGCAAGGAGATAAGAACAAGATTGTTACAGGAAGAG  
ACACACAGATGATTATTAATAATCTGAAAAGATGCTGAGTCTTACTCTAAGAAAAATTC  
ACATTTAACTACTCTGGGGGCTGGGCAAGGTGGCTCACGCCTGTAATCTCAACTGCG

27151 TCCTAAGAAAAATTCACATTTAACTACTCTGGGGGCTGGGCAAGGTGGCTCACGCCTGT  
AATCTCAACACTGGGAGACCAAGGCAGGAAGATCACTGAAGCCAGGGTATCGAGACCAGC  
CTGGACAACGTAGTGAGACCTTATCTCTTAAACAAAAACAAAACAAAACAAAAA  
AACAGTAAAAATTGGCCGGGCACAGTGACTCCTGCCTATAATCCCAGCACTTTGGGAAGC  
CCAGGTGAGTGGATCACTTGAGGTCAAGTGTGTTGAGAACAGCCTGGCCAACATGGCAAAA  
[C, T]  
TCCGTCTCTACTAAAAATTACAAAAATTAGCCAAGTGTGGTGGCATAAGCTGGTAGGGCA  
GCTACTTGGGAGGCTGATGTGAGACTCCATTTAAAAAATAAATCAAAAATTAGCTGGG  
TATAGTGGCACACCCCTATAGTTCTCGCTCCTTGGGAGGTTGAGGCAGGAGGATTGCCTG  
AGCCCAGGAGTTCAAGGCTGCAGTGAACCATGATCACACCACTGCATTCTAGCAGCCTGG  
GAGACAGAGCAAAACCTTGTCTCAAACAAACAAACAAACAAACAAAAACAAAAACACTT

28032 AGGAGCAGAGCCCTGCTCTTCTCATTCACTTACTTTATCTGTAAAATAGCATCATTTCTA  
CCACACGCTGGTGGTGTGAATAAAATGAGATGAAC'TCTAGCATAGAGTGCTTAGTAAAG  
GTTCTGGACATTTTCGTAGTAGTTGAATCATGCCAAATGTGGTCCTAGGTGATTGGCTTCT  
TTTGCTAGCATGTTTTAGGGCTCCTCCATGCTGGGGCATTGCATCACTGCTTTATTCCT  
TTTTATCGCCTAGTATTATTCCACTGTGTGGATAGACCACATTTATCCATTATCAGTTG  
[G, A]  
AGGATATTGGGTTCTTCCCATTTTTTTTGGCTATGGTGAATAGTACTGTGTACATTTGC  
ATATAAGGTTTGTGTAGATGTGTGTTTCCTTTTTCTGGGTCTATGCTGAGAAGTGA  
ATTGCTGGTTCATACAGCAGCTCGAACCTTGTGAGGAGCTGCCAGACGCTTTTCCAAGT  
CGCTCCACCATTTTACATTCCCGTCAGCAGTGTGAGAGTCCAGTTTACCAGCACTTGT  
TGTTATCTCTTTTAACTGTATGTATATATACTTAACATTTTATTTATAATAAATGTACA

28772 AAAATCATCAAGCCGAATCCCACTGTTAGAAATTAAGGTTTTATTTCATTTCAAGTTA  
TCAGGATCCAGGGAGGTGAATACACTTAGAGGATAGACTCAGCTCATTTCCAGCTATG  
CCTTTTCAGCAGCATTCTTACCAGAGTAGGAATATAATGTTAGTCATTATTTAGAGGCCCTG  
GCCATCTTGAGAAGGTTTACTGTTTAGTCTGCAGTACAATTATAACTGTTTTTGTATATT  
GGGTTATTTTTTTCAGAAGTAGGCCAGTAGCTCTAACAGGAGCCTCTTTAGCCTGAATTC  
[G, A]  
TCCAAGTAGTGCACTGTTGCACTAGTTGTCCCTCGGGACATGCTCCCCAATACGTAACTC  
ACTTCCAGGTTGCAACTGGACACTTACTGGTAGTCAGAAATAGCTATTGCATGGAGCTTA  
AAATGAACCTTGATCTTCGTGAAAGATGAGTCTGCAGCTAAGAGACTTTACTGTATATCAT

FIGURE 2U

AGTGTTTTTTTTTGTTTTGTTTTGTTTTGTTTTGTTGACGGAGTCTCACTCTTTCACCC  
AGGCTGGAGTGCAATGGCGAGATCTGACTCACTGCAACCTCCGCCCCCTAGGTTCAAGC

29572 TCATAGTTCTTATGCACAAAGACCCCTTAAATATTGTTTGTAATTTCTCCCCTATGCACAC  
GCTGACCTGTTTCTTAATCTTCTTATCTGTCTAGGTTTGGAGCAGGTATGTTAAGAAGTT  
AGGGGATTTTGCTAAGCCGGAGAATATTGACTTGCCCGTGCACTGCCTGAATGAACTTAT  
AACCAATGCACTGCACCACATCCAGATGTCATCACCTACCTTTTCGAGACTCAGAAACCA  
GAGTGTGTTTAACTTCTGTGCTATTCCACAGGTAGGGAACGGGGCTCCTCTGGGTGGATA  
[C, T]  
GGGGCTAAAGGGAGTGGGGTAGGAGTAAGGGTGGATTTTGCTGTGCTATATTCAAGGATA  
TGATTCTTAAAGACGATGACTCCAGTTTATTACGCTGGGAGTTTCATAGCACCCGCC  
TTTGCTTCCAGCCACCAACTCAGCTCAGCCTTGAGGTTAAGCCTGCTCCTTTTCAGAAC  
CTTCTTTCCGGATTTACTATTTTCTACAGCTATCCTAAACTAGTTAGGTTCTTTTCTCA  
CAGTTAAGTCAAGGTCTTTGGCTTAGATTTATGGGGAGTGCTGGGTAAACCTGGGTGAA

29761 ACTGCACCACATCCAGATGTCATCACCTACCTTTTCGAGACTCAGAAACCAGAGTGTGTT  
TAACCTCTGTGCTATTCCACAGGTAGGGAACGGGGCTCCTCTGGGTGGATACGGGGCTAA  
AGGGAGTGGGGTAGGAGTAAGGGTGGATTTTGCTGTGCTATATTCAAGGATATGATTCTT  
TAAAAAGACGATGACTCCAGTTTATTACGCTGGGAGTTTCATAGCACCCGCCCTTGCTTC  
CAGCCACCAAACTCAGCTCAGCCTTGAGGTTAAGCCTGCTCCTTTTCAGAACCTTCTTTC  
[C, T]  
GGATTACTATTTTCTACAGCTATCCTAAACTAGTTAGGTTCTTTTCTCACAGTTAAGT  
CAAGGTCTTTGGCTTAGATTTATGGGGAGTGCTGGGTAAACCTGGGTGAAGCTGTTATC  
ATTAAAAAGTCTTCATTAAGCACCTAATTACTGCTGTCTCTTTTCTAGACCCGGCATAAA  
AAGAACCTGGTCCGGTAGACCTAGCCTCTCAGTATGCTAGGAACCTACACTTTTTAGTTG  
CCTTTACCAAGTATTGCAGATACTACTGCAAATAAGTGAAGAAAGTAACAGCATTAACT

30732 ATTCTGTGTGTTGTTGAGAAAGGGAGGAGTGGGGAAGGTAAAAATCTTGACATACTTTCT  
TCGTGGGTATTTTTTCTTGAGCGATTCCATCTTAGTTGATTAGCAGTTAGCAATTGCCCA  
TTCAACAGAAGGTTTCTTACCTTTTGTGATAATGATAGCTAACGACATCATTTCTTCT  
TTTTTCCCTCTCTTCTGTTGTCTCTAGGTGATGGCCATTGCCACTTTGGCTGCCTGTTA  
TAATAACCAGCAGGTGTTCAAAGGGGCAGTGAAGATTCGGAAGGGCAAGCAGTGACCCT  
[G, C]  
ATGATGGATGCCACCAATATGCCAGCTGTCAAAGCCATCATATATCAGTATATGGAAGAG  
GTGGGTTTTTATTTAACTACTTGGATAATTTGTAGCTACTTTTATGATTTAGTAATGTCA  
CTGTTTAACCAGGTTTGGATATTAGATGATCCTAAACAATTCATATCCTGTGGCCTAAAG  
AGACAGGAATTGATATCCTTTATAAGGAAAAAAGTCTATTACAGGAGCCGAGCAGATTG  
CTCACTGCTGTGTAGTACCCTGGTGAGAGGAGATAAATGGAGCAAGGCTGTAGGTTGGAG

30841 GCAATTGCCCATTCACAGAAGGTTTCTTACCTTTTGTGATAATGATAGCTAACGACA  
TCATTTCTTCTTTTTTCCCTCTCTTCTGTTGTCTCTAGGTGATGGCCATTGCCACTTTG  
GCTGCCTGTTATAATAACCAGCAGGTGTTCAAAGGGGCAGTGAAGATTCGGAAGGGCAA  
GCAGTGACCCTGATGATGGATGCCACCAATATGCCAGCTGTCAAAGCCATCATATATCAG  
TATATGGAAGAGGTGGGTTTTTATTTAACTACTTGGATAATTTGTAGCTACTTTTATGAT  
[G, T]  
TAGTAATGTCACTGTTTAAACCAGGTTTGGATATTAGATGATCCTAAACAATTCATATCCT  
GTGGCTAAAGAGACAGGAATTGATATCCTTTATAAGGAAAAAAGTCTATTACAGGAGC  
CGAGCAGATTGCTCACTGCTGTGTAGTACCCTGGTGAGAGGAGATAAATGGAGCAAGGCT  
GTAGGTTGGAGCCCCCTCAGTAGAATCATAGATTTTGAGCTGCAAGATGATGCAGGAGGCC  
AACCAAGCTTCTTGTGCTGGTGAGGAATGTGAGGTTGAAGCTTGTCTGTGCTGATGCAG

31376 GAGGCCAACCAAGCTTCTTGTGCTGGTGAGGAATGTGAGGTTGAAGCTTGTCTGTGCTG  
ATGCAGTGCGTGATTGAGTGGATCTCTGGCTCCCGTCCATGTGTCTGACACCCAGTCTG  
GTACTTTCATTATGCCACAGGCCTCAATTGAAAAATCACAGTAGGGAATTTAGGCCAAGG  
AAAGCCATCAAGTTGCAATTATTTCTTAAATTTTCTTTGGAAAAATTCATTTCAAATACC  
AAAACCATCCTATAAAAAGAAAACCTTACCTTCTTAGGTCAAATCTCTAATATTTGACTAG  
[G, A]  
TTCAAAAAGTTTATTTCTGGCCAGGCACAGTAGCTTACTCCTGAAATCCCAGCACTTTGG  
GAGACCAAGGTGGGAGGATCACTTGAGGCCAGGAATTCAGACCAGCCGGGCGACATAG  
CAAGACCCCATTTCTACAAAAAATTTAAAAATTTGTCATGGTGGTGCACGCCTGTGGTCCC  
AGCTACTCAGGAGGCTGAGGCAGGTGGATCACATGAGCCTGAGAGGTGAGGCTACAGTA  
AGCTGTGTGATTTTCATCATTTGCACTCTAGCCTGGGTGATAGAGTGAGACTTTGTCTCAAA

FIGURE 2V

32032 TCTCTAGGCCCTAGAGCAGTGGTTTGTAAATGGAGGTGATTTGCTCCCCTCCCCCAGAG  
GACATTGGACAATGTCTGGAGACATTTTGGATTGTCTAACC GG CAGGAATCGGGTGCTA  
CTGGCATCTGGTGAGTAGAGGCCAGGATGATGCTGTGATCCTCAGGTGTGATCCTGTTG  
AGAATGAAACACTGTAGACTTTATGAAAACATACAAGACCCTCATCATTTTCCTTTGCC  
TGAGCTCCCTCCCAGAGGTTACCTCTGTTTCATGGTTTGTGCATCCGTCTAGTCCCCCT  
[A, G]  
TTACGCGTTTACAGGAATATGGTTTGCACAGTGTTCATCTAAATAGAATTATACAAA  
ATAGCGATTTCTGATTTCTCTTGCAATTTGCACATTCTTCTTATACTTCTCCCTACCTT  
TATCTGACACAGAAATGCTGTATGTCCAGAACTTCTATCAGAGGCACCTATGGAAGTCTA  
AGGGAAGACCACATCGCTTTTAAAAACCTAAAATTTGTAGTCACTAGATGAAAATATT  
CAGCCAGTGACCCAAAAAATTGCTACCAATGAGACTCTCCATTTTGCCATGTAGCCAGAA

32525 ATCGCTTTTAAAAACCTAAAATTTTGTAGTCACTAGATGAAAATATTAGCCAGTGACC  
CAAAAAATTGCTACCAATGAGACTCTCCATTTTGCCATGTAGCCAGAACTTACTTTGATC  
TATGTGCTGGGGTAGTGACCAAGTAGGTGGGTAGGAGTAATCTCAGGGAACTTGAGGC  
CCCAGCCTCATGGCTAGGGTCATAATTTGAACCCAGGTCTGTCTGACATCAGAAATCCATG  
ATGTTAACCCCAATTCTAAGGGGTTCAACTACCCTTTCTAAATGGAATCCTGCTATATTA  
[A, G]  
GCATATTTATTCAATTTATATAAACTAGAAACATTTTATGTAGTAAGTAGTTGAGAGTG  
TTTTGGTTTTGCAGTTTGATCACTAGTTTTAGAAACAGTTTTTAAACACTTTGTGGCCA  
ATTCCATTACTATATTAATTTAGATTTATTTGGTTTTCTTAACTATTGGGATTAAA  
TCCTGTTGTAAATTCATAGTTTGAAGGCGAGGGTGGCAGTCTACATTTGGCTGAGCCCT  
GTTTTGTGAATAAATGTTATCAGAACACAGCCACACCCATTTGCTTCTATGTCTTCTGT

34179 CTGCTGTATGTAGCACAGCATTGCACAAGAGCTTATTTAGTCTAGTAAACATTTATAGG  
AGCCTGTGTCAATTTAATCATCAAGCCTCGCACTGTGGCTCACACCTGTAATCCCAAAACT  
TTGGGAGGCTGAGGCAGGCAGATCACTTGAGGTAAGGAGTTCGAGACCAGCCTGGCCAAT  
ATGGCAAAACCTGTCTCTACTAAAAATACAACATTTAGCCAGGTGTGGTGGTGACACT  
TGTCATCCAGCTATTCGGAGCCTGAGACATGAGCATCGCTTGAACCTCGGGAGGTGGAG  
[G, T]  
TTGTAGTGAGCTGAGATGGCACCCTGCACTCCAGCCTGGGCAACAGGGTGAAGGCCCTT  
TCTCAAACTCCTCAAGTATTTGGCTTCAACTTTATGCGGGCATGTAGATGAAAAGTCCG  
CTATGACCTGTCTTTGACAAGCAGATGTAACCTCCTGATTGAGGCTAGTAGGTTTTAAG  
ACCTGAATAATTGAGTTTGAGAAACCTACTGTGTGCCTTCAGGTAAATGGAGAGTGGGG  
TTTGGTCTAGCAACGAAGCATCTAGAAGGTCTCTTTGGCCTTACCGGCTCTGTTTTAGGT

34249 ATTTAATCATCAAGCCTCGCACTGTGGCTCACACCTGTAATCCCAAAACTTTGGGAGGCT  
GAGGCAGGCAGATCACTTGAGGTAAGGAGTTCGAGACCAGCCTGGCCAATATGGCAAAAC  
CCTGTCTCTACTAAAAATACAACATTTAGCCAGGTGTGGTGGTGACACTTGTCAATCCCA  
GCTATTCGGAGCCTGAGACATGAGCATCGCTTGAACCTCGGGAGGTGGAGGTTGTAGTGA  
GCTGAGATGGCACCCTGCACTCCAGCCTGGGCAACAGGGTGAAGGCCCTTTCTCAAACT  
[T, C]  
CTCAAGTATTTGGCTTCAACTTTATGCGGGCATGTAGATGAAAAGTCCGCTATGACCTG  
TCCTTGACAAGCAGATGTAACCTCCTTGATTGAGGCTAGTAGGTTTTAAGACCTGAATAA  
TTGAGTTTGAGAAACCTACTGTGTGCCTTCAGGTAAATGGAGAGTGGGGTTTTGGTCTAG  
CAACGAAGCATCTAGAAGGTCTCTTTGGCCTTACCGGCTCTGTTTTAGGTAAGTCCACGT  
CTGAGTACCAGTGACTGCAGCTCTTCCAGTTGTGCTGTATGTTTATATGTTAGAAATGA

34451 GAGCATCGCTTGAACCTCGGAGGTGGAGGTTGTAGTGAGCTGAGATGGCACCCTGCACT  
CCAGCCTGGGCAACAGGGTGAAGGCCCTTTCTCAAACTCCTCAAGTATTTGGCTTCAACT  
TTATGCCGGGCATGTAGATGAAAAGTCCGCTATGACCTGTCTTGACAAGCAGATGTAAC  
TCCTTGATTGAGGCTAGTAGGTTTTTAAAGACCTGAATAATTGAGTTTGAGAAACCTACT  
GTGTGCCTTCAGGTAAATGGAGAGTGGGGTTTTGGTCTAGCAACGAAGCATCTAGAAGGTC  
[T, C]  
CTTTGGCCTTACCGGCTCTGTTTTAGGTAAGTCCACGTCTGAGTACCAGTGACTGCAGCT  
CTTCCAGTTGTGCTGTATGTTTATATGTTAGAAATGATCATCAAGGACTCAAAAGTTT  
TGCCACTAATTGTATTACCGGGGACTGTCACAACCAAGATTTCTCTAATTTATTCACCT  
TACTTATCTCCTGGAAGGCATATTGAAGTGCTCTTGAGTTCTCTAAAAGGGTTTTGTG  
TGGTTGTATATTCACTTGGGTGCCAGCGATTGATTCCAAATAAGTAAATCTTTTTTCC

34532 AGGCCCTTTCTCAAACTCCTCAAGTATTTGGCTTCAACTTTATGCGGGCATGTAGATGA

FIGURE 2W

AAAGTCGGCTATGACCTGTCTTGACAAGCAGATGTAACCTCTTGATTGAGGCTAGTAGG  
TTTTTAAGACCTGAATAATTGAGTTTGCAGAACTACTGTGTGCCTTCAGGTAAATGGA  
GAGTGGGGTTTGGTCTAGCAACGAAGCATCTAGAAGTCTCTTTGGCCTTACCGGCTCTG  
TTTTAGGTAAGTCCACGTCTGAGTACCAGTGACTGCAGCTCTTCCAGTTGTGCTGTCATG  
[T, C]  
TTATATGTTAGAAATGATCATCAAAGGACTCAAAAGTTTGGCCACTAATTGTATTACCGG  
GGACTGTCACAACCAAGATTTCTCTTAATTTATTCACCTTACTTATCTCCTGGAAGGGCA  
TATTGAAGTGCTCTTGGAGTTCTCTAAAAGGGTTTTTGTGGTTGTGTATATTCACTTGG  
GTGCCAGCGATTGATTCCAAATAAGTAAATCTTTTTTCCCAAAGGATGTAAGATGGCTT  
ATGGTTATAAGTACAACAGGCTAACAAAGTACAAGTAGATGAGAAAGTAAATGAAGAAA

36541 GGTAGGAGCCAGTTGAAGGGACGTGGGAGGCGCATTCAGAGAGAAGGAGTGGTATGAGA  
CTGGAACAGAGGTGTGCAGCAGCATCGCATGGGCGAAACAACAGTAGACAGTTGTTCTTT  
TGTTTTTGTGTTTTTTGAGACAGGGTCTTGTTCTGTCATCCAGGCTGGAGTGCAGTGG  
CATGATCTCGGATCACTGCAACCTCCACCTCCAGGCTCAAGTGATCTTCCACCCCAGT  
CCCCAAGTAGCTGGGGACCACAGGTGCATGCCACGATGCCCGGCTAATTTTTGTACATT  
[T, C]  
TGTAGAAAACAGGGTTTTACTGTGTTGTCCAGGCTGGTCTTAAACGCCTGAGCTTAAGCAG  
TCTACATGCCTCAGCCTCCTGAAGTGCTGGGATTCCAAACATGAGCCACTGTGCCTGGCCCGCAA  
CGGCAACTGTTACTAGACTATAGAGAGGGAGGTGGGCAAGGGCTGGTGACACTAGACAGG  
TGCAGTAGGTCTGGACCATGGGTGGCCTTGGCGCTACACATTACAGAGCTCAGGCTTTTTT  
TCTCCAGGTGAGAGGGCTGGTGCCACTGAGGCATCAAGCAGAGGTTTGAGATCTCCTTGG

36607 CAGAGGTGTGCAGCAGCATCGCATGGGCGAAACAACAGTAGACAGTTGTTCTTTTGTGTTT  
TGTTTTGTTTTTTGAGACAGGGTCTTGTTCTGTCATCCAGGCTGGAGTGCAGTGGCATGAT  
CTCGGATCACTGCAACCTCCACCTCCAGGCTCAAGTGATCTTCCACCCCAGTCCCCAA  
GTAGCTGGGGGACCACAGGTGCATGCCACGATGCCCGGCTAATTTTTGTACATTTTGTAG  
AAACAGGGTTTTACTGTGTTGTCCAGGCTGGTCTTAAACGCCTGAGCTTAAGCAGTCTAC  
[A, G]  
TGCCTCAGCCTCCTGAAGTGCTGGGATTCCAAACATGAGCCACTGTGCCTGGCCCGGCAA  
CTGTTACTAGACTATAGAGAGGGAGGTGGGCAAGGGCTGGTGACACTAGACAGGTGCAGT  
AGGTCTGGACCATGGGTGGCCTTGGCGCTACACATTACAGAGCTCAGGCTTTTTTCTCCA  
GGTGAGAGGGCTGGTGCCACTGAGGCATCAAGCAGAGGTTTGAGATCTCCTTGGTGACAG  
TGTAGAGCAGACAGGTAGATTGGGAATTTAAGCTTAGACTCACGTTGGAGACTGAGATA

36681 GACAGGGTCTTGTTCTGTCATCCAGGCTGGAGTGCAGTGGCATGATCTCGGATCACTGCA  
ACCTCCACCTCCCAGGCTCAAGTGATCTTCCACCCCAGTCCCCAAGTAGCTGGGGGACC  
ACAGGTGCATGCCACGATGCCCGGCTAATTTTTGTACATTTTGTAGAAACAGGGTTTTAC  
TGTTTGTGCCAGGCTGGTCTTAAACGCCTGAGCTTAAGCAGTCTACATGCCTCAGCCTCC  
TGAAGTGCTGGGATTCCAAACATGAGCCACTGTGCCTGGCCCGGCAACTGTTACTAGACT  
[A, G]  
TAGAGAGGGAGGTGGGCAAGGGCTGGTGACACTAGACAGGTGCAGTAGGTCTGGACCATG  
GGTGGCCTTGGCGCTACACATTACAGAGCTCAGGCTTTTTTCTCCAGGTGAGAGGGCTGG  
TGCCACTGAGGCATCAAGCAGAGGTTTGAGATCTCCTTGGTGACAGTGTAGAGCAGACAG  
GTAGATTTGGGAATTTAAGCTTAGACTCACGTTGGAGACTGAGATAGCTCATCTGAGAGG  
CACTCAGGCGCTAATCTCAGGCAGTAATTTAGGGATGTAGGGGAAGAGATGGATTCTGC

37493 TGACGTTTATTGGGCCTGGCACTGTGAGGTGCTGGGGATGTGAAGATCATTGTGGCTCAG  
CCGCTGCTCTCGAGGGCTCTGGGTGCAGTATGCACACCTGTGCCTCCTGTTTGCTCAGG  
AAGACAGGCTTTGAGATGAGCTGGGGCTGACATCCCCACCTTATCATTGGGATGGCTTG  
GGTAAGTTATGTTTATGTTCTCTGAGCCTCCCTTTCTCATTGGTAAAATGGGTATAAAA  
TACCTGCCAGTGAGGGTTGTTGTAAGTAGCCATGGAAAATGTAAAGCACATAGCACTTA  
[C, T]  
CATTTTTTCTGTGTCTTTAAACAGATTTATCATAGAATCCCCGACTCAGACCCATCTTCT  
AGCAAAACAAGGCAGATCATCTCCACCATCCGGACGAGAATCTTCCCAACTGTCAGCTG  
ATTTCCCGAAGCCACTACTCCCCCATCTACCTGTGCTTTGTGTCATGCTTTTGGCTGCCTG  
AGCTGGCAGTACCTGACCACTCTCTCCAGGTAACAGAAGACTATGTTTCAGACTGGAGAA  
CACTGATCCCAAATTTGTCCATAGCTGAAGTCCACCATAAAGTGGATTACTTTTTTCT

37966 CTGCCCTGAGCTGGCAGTACCTGACCACCTCTCTCCAGGTAACAGAAGACTATGTTTCAGA  
CTGGAGAACTGATCCCAAATTTGTCCATAGCTGAAGTCCACCATAAAGTGGATTACT  
TTTTTTCTTTAAGGATGGATGTTGTGTTCTCTTTATTTTTTCTACTACTTTAATCCCT

FIGURE 2X

AAAAGAACGCTGTGTGGCTGGGACCTTTAGGAAAGTGAAATGCAGGTGAGAAGAACCTAA  
ACATGAAAGGAAAGGGTGCCTCATCCAGCAACCTGTCTTGTGGGTGATGATCACTGTG  
[C, A]  
TGCTTGTGGCTCATGGCAGAGCATTCACTGCCACGGTTTAGGTGAAGTCGCTGCATATGT  
GACTGTGATGAGATCCTACTTAGTATGATCCTGGCTAGAATGATAATTAAAAGTATTTAA  
TTTGAAGCACCATTGTAATGTTTCGTACTAGTAGAAAATGATGTGAATTTCTTTCTGTTC  
GGCTCCTATTTTCTCATCATTTTGTTCCTTAATTGGGTTGAATGGAGTAGATAGAAA  
TATTTATGGTTTAGGTAACAGTTAGATGTTTCTAAGAATGCAAACTGCCTTTTCCACAC

37973 GAGCTGGCAGTACCTGACCACTCTCTCCCAGGTAACAGAAGACTATGTTTCAGACTGGAGA  
ACACTGATCCCAAATTTGTCCATAGCTGAAGTCCACCATAAAGTGGATTACTTTTTTTC  
TTTAAGGATGGATGTTGTGTTCTCTTTATTTTTTCTTACTACTTTAATCCCTAAAAGAA  
CGCTGTGTGGCTGGGACCTTTAGGAAAGTGAAATGCAGGTGAGAAGAACCTAAACATGAA  
AGGAAAGGGTGCCTCATCCAGCAACCTGTCTTGTGGGTGATGATCACTGTGCTGCTTG  
[T, C]  
GGCTCATGGCAGAGCATTCACTGCCACGGTTTAGGTGAAGTCGCTGCATATGTGACTGTC  
ATGAGATCCTACTTAGTATGATCCTGGCTAGAATGATAATTAAAAGTATTTAATTTGAAG  
CACCATTGAATGTTTCGTACTAGTAGAAAATGATGTGAATTTCTTTCTGTTCCGGCTCCT  
ATTTTCTCATCATTTTGTTCCTTTAATTGGGTTGAATGGAGTAGATAGAAAATATTTAT  
GGTTTAGGTAACAGTTAGATGTTTCTAAGAATGCAAACTGCCTTTTCCACACAAAGGCT

38113 TCTCTTTATTTTTTCTTACTACTTTAATCCCTAAAAGAACGCTGTGTGGCTGGGACCTT  
TAGGAAAGTGAAATGCAGGTGAGAAGAACCTAAACATGAAAGGAAAGGGTGCCTCATCCC  
AGCAACCTGTCTTGTGGGTGATGATCACTGTGCTGCTTGTGGCTCATGGCAGAGCATT  
AGTGCCACGGTTTAGGTGAAGTCGCTGCATATGTGACTGTGATGAGATCCTACTTAGTAT  
GATCCTGGCTAGAATGATAATTAAAAGTATTTAATTTGAAGCACCATTGAATGTTTCGTA  
[C, A]  
TAGTAGAAAATGATGTGAATTTTCTTCTGTTCCGGCTCCTATTTTTCTCATCATTTTGT  
TTCTTTAATTGGGTTGAATGGAGTAGATAGAAAATATTTATGGTTTAGGTAACAGTTAGAT  
GTTTCTAAGAATGCAAACTGCCTTTTCCACACAAAGGCTGGGAATAAAATTCTGGGTAT  
TCTCGTATTCTCATTTAAAGGAGTTTAGCTTTTCTAGAGAGAAACAGCAGGATTGCTTTTGA  
CCTTTTAGAAGATTGGTCTCCAGTAAAGGTGGACATTTTGTAGATTTTATAATAAAGAA

38298 CACGGTTTAGGTGAAGTCGCTGCATATGTGACTGTGATGAGATCCTACTTAGTATGATCC  
TGGCTAGAATGATAATTAAAAGTATTTAATTTGAAGCACCATTGTAATGTTTCGTACTAGT  
AGAAAATGATGTGAATTTCTTTCTGTTCCGGCTCCTATTTTCTCATCATTTTGTTCCT  
TTAATTGGGTTGAATGGAGTAGATAGAAAATATTTATGGTTTAGGTAACAGTTAGATGTT  
CCTAAGAATGCAAACTGCCTTTTCCACACAAAGGCTGGGAATAAAATTCTGGGTATTCTC  
[G, C]  
TATTCTCATTTAAAGGAGTTTAGCTTTTCTAGAGAGAAACAGCAGGATTGCTTTTGACCTT  
TAGAAGATTGGTCTCCAGTAAAGGTGGACATTTTGTAGATTTTATAATAAAGAATTTAA  
TTGCTCTGCATTTGTCAAGTACAGTTTCGCTTGAAGCCTGCCTGACTGTGAAAAGATGG  
AGCTCAAGAATGGAGTTGATGGCCACGCTGGTGGCTCATGCCTGTAATCCAGCACTTT  
GGGAGGCTGAGGCGGTTCGGATCACGACATTAGGGGATCGAGACCATCCTGGCTAACACGG

FIGURE 2Y